United States Utility Patent Application

of

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for

DIFFERENTIALLY-EXPRESSED CONIFER cDNAs, AND THEIR USE IN IMPROVING SOMATIC EMBRYOGENESIS

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CROSS-REFERENCE TO RELATED APPLICATIONS

[001] This patent application claims benefit of priority of provisional application U.S. Ser. No. 60/239,250, filed October 11, 2000, and claims benefit of priority of provisional application U.S. Ser. No. 60/260,882, filed January 12, 2001.

FIELD OF THE INVENTION

[002] The present invention relates to a relational database of cDNA molecules, including those corresponding to Loblolly Pine Major Intrinsic Protein (MIP), which are differentially expressed during plant embryogenesis. The present invention further relates to the use of DNA arrays for evaluating gene expression in somatic and zygotic embryos. The invention encompasses related nucleic acids, proteins, antigens, and antibodies derived from these cDNAs as well as the use of such molecules for the staging, characterization, and manipulation of plant embryogenesis, in particular conifer embryogenesis. The cDNAs and related nucleic acids, proteins, antigens, and antibodies derived from these cDNAs are useful in the design, selection, and cultivation of improved crops, specifically including coniferous trees, which provide raw materials for paper and wood products.

BACKGROUND OF THE INVENTION

[003] The world demand for paper is expected to increase nearly 50% by the year 2010 (McNutt and Rennel, *Pulp Paper Intern* 39: 48 (1997)). The United States' forest products industry faces a great challenge in order to keep pace with the growing demand for paper. This challenge is made greater by the decreasing availability of a forest land-base, resulting from environmental restrictions and urban growth, from which to harvest timber resources. Additionally, valuable wood resources are lost to the

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environmental stresses and biotic diseases. Consequently, the push to secure a renewable and sustainable source of raw material for paper and other wood related products has become an important priority for the forest products industry.

[004] Current forestry related research and development is focused on creating sustainable fiber farms or tree plantations. Farming trees with elite germplasms will increase growth rates and yields of wood per acre. However, creating improved tree stock requires the ability to identify and generate genetically superior trees and a way to propagate such superior trees without diluting their genetic quotient.

A. Breeding and Selection

[005] Addressing the need to propagate genetically superior trees without genetic diminution demands full research attention. Traditional methods of tree propagation relied on selected breeding programs to achieve genetic gain, i.e., the development of a strain, sub-strain, or line having any heritable and economically valuable characteristic or combination of characteristics not found in the parents. Based on the results of progeny tests, superior maternal trees are selected and used in "seed orchards" for mass production of genetically improved seed. The genetic gain in such an open-pollinated sexual propagation strategy is, however, limited by the breeder's inability to control the paternal parent. Additional gains can also be achieved by control-pollination of the maternal tree with pollen from individual trees whose progeny have demonstrated superior growth characteristics. Nevertheless, even under controlled conditions where both parents of each seed are the same, sexual propagation results in a "family" of seeds, i.e., siblings, comprised of many different genetic combinations. As not all genotype combinations are favorable, the genetic gain

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in any particular progeny is frequently offset and obscured by the genetic variation among sibling seeds and those seedlings retaining undesirable or previously masked pre-cross traits.

[006] In addition to inherent genetic limitations of a traditional breeding programs, large-scale production of control pollinated seeds is also expensive. Consequently, economic and biological limitations of large-scale seed production has lead the industry to turn towards methods of asexual reproduction, such as grafting, vegetative propagation and micropropagation, as more viable alternatives.

B. Asexual (Clonal) Propagation

[007] Asexual propagation permits the application of very high selection intensity, resulting in the propagation of only those progeny showing a high genetic gain potential. These highly desirable progeny can have unique genetic combinations that result in superior growth and performance characteristics. Thus, with asexual propagation it is possible to genetically select individuals while avoiding a concomitant reduction of genetic gain due to intra-familial variation.

[008] Asexual propagation of trees can be accomplished currently by grafting, vegetative propagation, and micropropagation. Grafting, widely used to propagate select individuals in limited quantities for seed orchard establishment, is not applicable to large-scale production for reforestation. Vegetative propagation, achieved by the rooting of cuttings, and micropropagation by somatic embryogenesis, currently hold the most potential for reforestation of conifers. Although vegetative propagation by rooted cuttings can be achieved in many coniferous species, large-scale production via this method is extremely costly due to difficulties in automating and mechanizing the

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process, not to mention the need for tremendous quantities of stock tissue. This propagation method is still further limited by the fact that the rooting potential of stock plants decrease with time, making it difficult to serially propagate from select genotypes over extended periods of time.

[009] Micropropagation is the most promising method of asexual propagation for mass plantings. This process involves the production of somatic embryos *in vitro* from minute pieces of plant tissue or individual cells. The embryos are referred to as somatic because they are derived from the somatic (vegetative) tissue, rather than from the sexual process. Both vegetative propagation and micropropagation have the potential to capture all genetic gain of highly desirable genotypes. However, unlike conventional vegetative propagation methods, somatic embryogenesis is amenable to automation and mechanization, making it highly desirable for large-scale production of planting stock for reforestation. Moreover, somatic embryogenesis is particularly amenable to high intensity selection of a large number of clones. These advantages are compounded by the ability to safely preserve somatic embryogenic cultures in liquid nitrogen for long-term storage. Consequently, long-term cryogenic preservation offers immense advantages over other vegetative propagation systems that attempt to maintain the juvenility of stock plants. Techniques for somatic embryogenesis in a wide variety of plant species are well known in the art; exemplary methods for performing somatic embryogenesis in conifers are taught in U.S. Patents: 5,036,007; 5,236,841; 5,294,549; 5,413,930; 5,491,090; 5,506,136; 5,563,061; 5,677,185; 5,731,203; 5,731,204; and 5, 856,191, herein incorporated by reference in their entirety.

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[010] Thus, somatic embryogenesis has great potential for clonal production of conifer embryos to meet the increased demands of the pulp and paper industry. Assessment of embryo quality, however, needs improvement. The process of creating better tree stock begins with understanding the process of tree development from embryogenesis through full maturation.

[011] In general, plant tissue culture is the broad science of growing plant tissues on or in a nutrient medium containing minerals, sugars, vitamins and plant hormones. By adjusting the composition of the media, cultured tissues can be induced to grow or differentiate into specific cell types or organs. "Somatic embryogenesis" is a type of plant tissue culture where a piece of a donor plant is excised, cultured and induced to form multiple embryos. An embryo is a discrete mass of cells with a well-defined structure that is capable of growing into a whole plant.

[012] The methods generally in use for somatic embryogenesis today involve several steps. Prior to the tissue culture process, a suitable "explant" is harvested. A typical explant in conifer somatic embryogenesis is the "megagametophyte", a haploid nutritive tissue of the conifer seed, which is extracted from the ovule of a pollinated female cone. This ovule contains single or multiple zygotic seed embryos. In the seeds of many coniferous species, one or more genetically unique embryos naturally undergo a process called cleavage polyembryony, where a zygotic embryo grows and divides to form a small clones of embryos.

[013] The first step in somatic embryogenesis is the initiation step. The explant is placed on a suitable media. When the explant is an ovule, a process called extrusion occurs. Extrusion involves the emergence or expulsion of a zygotic embryo or multiple

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embryos and embryogenic tissue out of the megagametophyte. If culture conditions are suitable, initiation proceeds and the extruded embryo or embryos undergo the process of cleavage polyembryony. This results in the formation of early stage somatic embryos in a glossy, mucilaginous mass.

[014] After embryogenic cultures are initiated, the somatic embryos are transferred to a second medium with an appropriate composition of plant hormones and other factors to induce the somatic embryos to multiply. In the multiplication stage, cultures can double up to 2-6 times in one week. Once large numbers of embryos are obtained in the multiplication stage, the embryos are moved to a development and maturation medium. Here, the correct balance of plant hormones and other factors will induce the early-stage embryos to mature into late stage embryos. Following the maturation and development stage, embryos are germinated to form small seedlings. These seedlings are then acclimated for survival outside of the culture vessel. After acclimation, the seedlings are ready for planting.

[015] The relative ability to propagate plants by somatic embryogenesis can vary greatly between species. Among conifers, for example, spruce (*Picea*) species and Douglas fir are easily propagated, while *Pinus* species are much more difficult. Many *Pinus* species, including Loblolly pine (*Pinus taeda*), do not readily initiate embryonic cultures. Typical initiation frequencies between 1% and 12% are reported for various *Pinus* species (Becwar et al., *For. Sci.* p1-18 (1988), Jain et al., *Plant Sci.* 65:233-241 (1989), Becwar et al., *Can. J. For. Res.* 20:810 (1990), Li and Huang, *J. Tissue Cult. Assoc.* 32:129 (1996)). Laine and David, (*Plant Sci.* 69:215 (1990)), however, were able to obtain high frequencies of initiation (up to 59%) in *Pinus*

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caribaea, suggesting that not all *Pinus* species are recalcitrant. Also, one earlier report described initiation frequencies of 54% in White pine (*Pinus strobus*). Finer et al., *Plant Cell Rep.* 8:203 (1989). However, other workers were not able to duplicate this success. Michler et al., *Plant Sci.* 77:111 (1991). The results in the literature demonstrate the recalcitrance of *Pinus* species, especially Loblolly pine, in regeneration by somatic embryogenesis.

[016] Nevertheless, once this process is understood from the standpoint of developmental genetics, breeders will then have the appropriate tools to monitor, intervene, and improve both the regeneration frequency and the overall quality of tree stock through genetic engineering. For example, both environmental requirements and responsiveness of a developing embryo change as the embryo passes various developmental milestones. Consequently, accurate and timely knowledge of the developmental stage of an embryonic culture would allow the skilled practitioner to beneficially adjust the growth media components and other environmental factors to achieve optimal embryo survival, growth, and maturation. In addition, an understanding of developmentally regulated genes would allow for early selection of advantageous clones and provide tools for developmentally regulated transgenic expression systems.

[017] Currently, a reasonable determination of the precise developmental stage of an embryo requires a practiced, physical familiarity with the morphological appearance of embryos at different stages, which is further complicated by the presence of morphological variations between species. Consequently, visual determination is performed best by experts in the field. Thus, there is a need in the art for a staging method which can be reliably practiced by the ordinary practitioner. The

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current invention will allow one to stage embryos based on a relational database system profiling gene expression patterns instead of physical morphological differences, thereby permitting one less skilled in the art of visual staging to biologically determine the stages of embryogenesis.

[018] The traditional morphological staging method provides only a crude indication of the underlying biochemical condition or state of an embryo. This level of information is insufficient for refining culture conditions, including media formulations, or for selecting potentially advantageous embryo clones for further development. Thus, there is a need in the art for a more sensitive staging method that precisely defines the physiological age, health, growth requirements, and potential fitness of a particular embryo. The current invention will allow definitive staging significantly beyond that currently practiced in the art, and provides a detailed analysis of the biochemical state and potential fitness of an embryo by comparison to developed relational database profiles.

[019] Visual staging methods depend on morphological markers to assign a numerical stage of 1-9 to an embryo. Nevertheless, it is well accepted that visually undetectable developmental changes occur in an embryo after it reaches stage 9. The current invention is particularly useful in providing means for monitoring and evaluating the developmental state of these older embryos, as genetic responses occur and are detectable up to and through an adult tree's life.

[020] There further exists in the art a need for information regarding the proteins, genes, and gene expression patterns in plant embryo development, as well as a more thorough understanding of how this information relates to the physiology,

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developmental potential, and genetic quotient of a plant embryo. The relational database system provides a platform for which to monitor individual gene expression levels during embryo development while directly correlating expression with, for example, environmental conditions, age, and embryo fitness, as well as the protein identification achieved by BLAST searches of publicly available databases (i.e., GenBank) for desirable genes. Accordingly, the present invention therefore provides the additional ability to correlate the direct, global gene expression response within the embryo system to a typically non-expressing gene driven by a stage-specific promoter.

SUMMARY OF THE INVENTION

[021] The present invention addresses these needs by providing in a relational database format nucleic acid and protein sequences that are differentially expressed during various stages of plant embryogenesis. The invention encompasses a set of isolated nucleic acid molecules comprising the DNA sequence of any one of SEQ ID NOS: 1-334 and nucleic acid molecules related or complementary to any one of SEQ ID NOS: 1-334. (See Table I) As such, the invention includes both single-stranded and double-stranded RNA and DNA nucleic acids, including variants thereof. The nucleic acids of the invention can be used as an expression template in the form of DNA arrays, including for example, gene arrays, DNA chips, and dot array Southerns, for which to compare and evaluate expression in test samples. (See Table II) The nucleic acids of the invention can be further used as probes to detect the presence or level of both single-stranded and double-stranded RNA and DNA encoding variants of polypeptides or fragments of polypeptides encompassed by the invention. The nucleic acids of the invention can be further used as promoters for the expression of sense and antisense

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molecules at specific stages of embryo development. Data acquired through the use of the present invention can in turn be provided to the relational database for further development.

[022] Isolated nucleic acid molecules that hybridize to a denatured, double-stranded DNA comprising the DNA sequence of any one of SEQ ID NOS: 1-334 under conditions of moderate or high stringency are also encompassed by the invention. The invention further encompasses synthetic and naturally-occurring variants of the nucleic acids described in SEQ ID NOS: 1-334, for example, isolated nucleic acid molecules derived by *in vitro* mutagenesis from SEQ ID NOS: 1-334. *In vitro* mutagenesis would include numerous techniques known in the art including, but not limited to, site-directed mutagenesis, random mutagenesis, and *in vitro* nucleic acid synthesis.

[023] The invention also encompasses related molecules (variants) including isolated nucleic acid molecules degenerate from SEQ ID NOS: 1-334 as a result of the genetic code, for example, naturally-occurring or synthetic allelic variants of the genes encoding SEQ ID NOS: 1-334. Such related molecules also encompass both smaller and larger nucleic acids that contain sufficient sequence to support hybridization to any of SEQ ID NOS: 1-334 under conditions of moderate or high stringency. Consequently, recombinant vectors, including those that direct the expression of these nucleic acid molecules and host cells transformed or transfected with these vectors are herein defined as variants and are encompassed by the invention.

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[024] Another embodiment of this invention is the production of transgenic vectors and transgenic plants comprising vectors or other nucleic acids comprising any

one of SEQ ID NOS: 1-334 and related molecules. Particularly preferred are those capable of expressing polypeptides or peptides encoded by any of SEQ ID NOS: 1-327. In a preferred embodiment, the transgene comprises SEQ ID NO: 327, or a variant thereof.

[025] SEQ ID NO: 327 encodes a protein which corresponds to a novel Loblolly pine homolog of the plant Major Intrinsic Protein (MIP) family. MIPs comprise a large family of related proteins that function as membrane channels for the transport of water and possibly ions across cellular membranes. Henceforth, the encoded protein of SEQ ID NO: 327 may be referred to as Loblolly MIP. Variants, including naturally-occurring and artifactually-programmed allelic variants, vectors, and other nucleic acids which hybridize to SEQ ID NO: 327 under conditions of moderate or high stringency are encompassed by the invention. Also encompassed are plant cells, seeds, embryos and trees, transgenic for loblolly pine MIP, and variants thereof.

[026] The invention also encompasses isolated polypeptides, or fragments thereof, encoded by any one of the nucleic acid molecules of SEQ ID NOS: 1-327, including variants thereof. The invention further encompasses the use of these peptide sequences as markers for staging, monitoring, and selecting embryos and embryo cultures. The invention also encompasses methods for the production of these polypeptides or fragments thereof including culturing a host cell under conditions promoting expression and recovering the polypeptide or peptide from the culture medium. In particular, the expression of polypeptides or peptides encoded by SEQ ID NOS: 1-327 in viral vectors, bacteria, yeast, plant, and animal cells is encompassed by

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the invention. Isolated polyclonal or monoclonal antibodies that bind to peptides encoded by SEQ ID NOS: 1-327 are also encompassed by the invention.

[027] Further encompassed by this invention are methods for using the nucleic acid molecules of any one of SEQ ID NOS: 1-327 to obtain full length cDNA and genomic sequences of the corresponding genes, including cognate, homologous, or otherwise related genetic sequences, which hybridize to any of SEQ ID NOS: 1-327 under conditions of moderate or high stringency. Also provided by this invention are oligonucleotides derived from any one of SEQ ID NOS: 1-334 that can be used as probes and/or as primers in PCR, RT-PCR, and other assays to detect the presence or level of the nucleic acids of SEQ ID NOS: 1-334 and related molecules.

[028] The primers and other probes of the invention may be used to monitor and characterize the development of plant embryos, in particular, pine tree embryos. Characterization of embryonic gene expression provides means for correlating gene expression with current and potential plant phenotypes. Consequently, the present invention encompasses means for monitoring and adjusting growth conditions (see Figure 6), as well as means for selecting genetically superior embryonic clones for further propagation and expansion (see Figure 8). Thus, the present invention encompasses the use of DNA or RNA probes derived from the nucleic acid molecules of SEQ ID NOS: 1-334 in any form, e.g., in DNA arrays, and antibodies raised against polypeptides or peptide fragments encoded by SEQ ID NOS: 1-327, to determine relative or absolute levels of expression of the genes or proteins encoded by SEQ ID NOS: 1-327. In addition, these nucleic acid and antibody probes may be used for

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staging, monitoring, characterizing, or selecting plant embryos or embryo cultures, particularly pine tree embryos.

[029] The relational database of the present invention allows expression information pertaining to embryo stages to be viewed as sequence data generated in accordance with the present invention. The invention includes a database for storing a plurality of sequence records for which to correlate embryo stages to sequence records. The method further involves providing an interface which allows a user to select one or more expression categories contained within the database.

[030] The relational database is designed to include separate parts or cells for information storage. One cell or part may contain a gene expression database which contains nucleic acid molecules of SEQ ID NOS: 1-327. Other cells or parts may contain descriptive information pertaining to each nucleic acid molecules of SEQ ID NOS: 1-327, additional sequence data related to the gene expression database, protein encoded by nucleic acids disclosed herein, similarity values to known proteins of other systems, and to conditions under which expression data was obtained.

[031] The database system described in the present invention will allow identification or selection of particular genes of interest for further use with DNA arrays. Identification or selection of particular genes may include, for example, those related to patterns of expression, those identified with homology to known genes from other studies, and those sequences considered novel.

BRIEF DESCRIPTION OF THE DRAWINGS

[032] FIG. 1 depicts differential display of loblolly pine zygotic and somatic embryos at different stages of development.

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[033] FIG. 2 displays embryo gene expression observed by high-density array Southern hybridization.

[034] FIG. 3 provides a general schematic for gene regulation studies arising from the cDNA cloning of genes expressed in embryos.

[035] FIG. 4 depicts graphical representation of hybridization of 'dehydrin' and LPZ216 cDNA probes to total RNA isolated from zygotic embryos of loblolly pine.

[036] FIG. 5 displays ABA concentration of loblolly pine embryos.

[037] FIG. 6 shows schematic of gene study for improved somatic embryogenesis.

[038] FIG. 7 shows detection of gene expression by high-density array Southern hybridization for loblolly pine genotype 333 after 12 weeks on two maturation media.

[039] FIG. 8 depicts the application of embryogenic gene expression studies.

[040] FIG. 9 displays slot blots and expression levels for three embryogenesis-related genes.

FIG. 10 depicts clone LPS-097 sequence (LP2-3 differential display fragment.)

FIG. 11 displays a northern blot for the LP2-3 gene during stages 1-3.

FIG. 12 displays a slot blot of total RNA from somatic embryo tissue probed with an LP2-3-specific probe.

FIG. 13 displays a slot blot of total RNA from zygotic embryo tissue probed with an LP2-3-specific probe.

[041] FIG. 14 depicts the quantified expression of early zygotic embryos compared to early somatic embryos.

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DETAILED DESCRIPTION OF THE INVENTION

[042] The three hundred and twenty-seven differentially expressed cDNAs isolated from plant specimens of known developmental ages are disclosed in SEQ ID NOS: 1-327. The seven stage-specific promoters isolated from plant specimens are disclosed in SEQ ID NOS: 328-334. The discovery of these cDNAs and promoters enables the design, isolation, and construction of related nucleic acids, proteins, antigens, antibodies other heterologous genes. Both the cDNAs and promoters facilitate the staging, characterization, and manipulation of plant embyrogenesis, in particular, conifer embryogenesis. These molecules, and related nucleic acids, peptides, proteins, antigens, and antibodies are particularly useful when compiled into a relational database for the monitoring, design, selection, and cultivation of improved crop plants.

[043] The cDNAs of SEQ ID NOS: 1-327, in addition to the promoters of SEQ ID NOS: 328-334, were originally derived from Pinus taeda embryos, commonly known as the Loblolly Pine. Nevertheless, it is understood that the invention is applicable to and encompasses all plants, including all dicotyledonous plants, including all conifers, including all species of Pinus, Picea, and Pseudotsuga. Exemplary conifers may include Picea abies, and Psedotsuga menziesii, and Pinus taeda.

Nucleic Acid Molecules

[044] In a particular embodiment, the invention relates to certain isolated nucleotide sequences including those that are substantially free from contaminating endogenous material. The terms "nucleic acid" or "nucleic acid molecule" refer to a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form,

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and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides. A "nucleotide sequence" also refers to a polynucleotide molecule or oligonucleotide molecule in the form of a separate fragment or as a component of a larger nucleic acid. The nucleotide sequence or molecule may also be referred to as a "nucleotide probe." The nucleic acid molecules of the invention are derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequence by standard biochemical methods. Examples of such methods, including methods for PCR protocols that may be used herein, are disclosed in Sambrook et al., *MoLecular Cloning: A Laboratory Manual,* 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989), *Current Protocols in Molecular Biology* edited by F.A. Ausubel et al., John Wiley and Sons, inc. (1987), and Innis, M. et al., eds., *PCR Protocols: A Guide to Methods and Applications*, Academic Press (1990), each of which are herein incorporated by reference in their entirety.

[045] As used herein a "nucleotide probe" is defined as an oligonucleotide capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, through complementary base pairing, or through hydrogen bond formation. As described above, the oligonucleotide probe may include natural (ie. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, bases in a oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, so long as it does not prevent hybridization. Thus,

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oligonucleotide probes may have constituent bases joined by peptide bonds rather than phosphodiester linkages.

[046] A "target nucleic acid" herein refers to a nucleic acid to which the nucleotide probe or molecule can specifically hybridize. The probe is designed to determine the presence or absence of the target nucleic acid, and the amount of target nucleic acid. The target nucleic acid has a sequence that is complementary to the nucleic acid sequence of the corresponding probe directed to the target. As recognized by one of skill in the art, the probe may also contain additional nucleic acids or other moieties, such as labels, which may not specifically hybridize to the target. The term target nucleic acid may refer to the specific nucleotide sequence of a larger nucleic acid to which the probe is directed or to the overall sequence (e.g., gene or mRNA) whose expression level it is desired to detect. One skilled in the art will recognize the full utility under various conditions.

[047] As described herein, the nucleic acid molecules of the invention include DNA in both single-stranded and double-stranded form, as well as the RNA complement thereof. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. Genomic DNA, including translated, non-translated and control regions, may be isolated by conventional techniques, *e.g.*, using any one of the cDNAs of SEQ ID NO: 1 through SEQ ID NO: 327, or suitable fragments thereof, as a probe, to identify a piece of genomic DNA which can then be cloned using methods commonly known in the art. In general, nucleic acid molecules within the scope of the invention include sequences that hybridize to sequences of SEQ ID NOS: 1-334 under hybridization and wash conditions of 5°, 10°,

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15°, 20°, 25°, or 30° below the melting temperature of the DNA duplex of sequences of SEQ ID NOS: 1-334, including any range of conditions subsumed within these ranges.

DNA Arrays

[048] In a further embodiment, DNA arrays are used to identify hybridizing sequences from test samples. The term "DNA array" refers to "gene arrays," "DNA chips," "dot array Southerns," etc. One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The DNA array will typically include one or a multiplicity of nucleic acid molecules derived from SEQ ID NO: 1 through SEQ ID NO: 327 that specifically hybridize to the nucleic acid expression of which is to be detected. In addition, the array may include one or more control probes to monitor the expression system. Control probes refer to known expression products present at each stage of expression, e.g., ribosomal gene products or the transcripts of other housekeeping genes. The organization of the DNA array will be known to facilitate interpretation of results. Examples in the art describing the uses and composition of DNA arrays can be found in U.S. Patents: 5,700,637, 5,837,832, 5,843,655, 5,874,219, 6,040,138, 6,045,996, and are incorporated by reference.

Molecules That Hybridize to Identified Sequences

[049] Thus, in a particular embodiment, this invention provides an isolated nucleic acid molecule selected from the group consisting of:

(1) a DNA sequence comprising any one of the sequences presented in SEQ ID NO: 1 through SEQ ID NO: 334;

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(2) an isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of (a) under conditions of moderate stringency; and

(3) an isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of (a) under conditions of high stringency.

[050] As used herein, stringency conditions in nucleic acid hybridizations can be readily determined by those having ordinary skill in the art based on, for example, the length and composition of the nucleic acid. In one embodiment, moderate stringency is herein defined as a nucleic acid having 10, 11, 12, 13, 14, 15, 16, or 17, contiguous nucleotides identical to any of the sequences of SEQ ID NOS: 1-334, or a complement thereof. Similarly, high stringency is hereby defined as a nucleic acid having 18, 19, 20, 21, 22, or more contiguous identical nucleotides, or a longer nucleic acid having at least 80, 85, 90, 95, or 99 percent identity with any of the sequences of SEQ ID NOS: 1-334; for sequences of at least 50, 100, 150, 200, or 250 nucleotides, high stringency may comprise an overall identity of at least 60, 65, 70 or 75 percent.

[051] Generally, nucleic acid hybridization simply involves providing a denatured nucleotide molecule or probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. The nucleic acids that do not substantially form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is further generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration

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of the buffer containing the nucleic acids. Under lower stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

[052] As used herein, the percent identity between an amino acid sequence encoded by any of SEQ ID NOS: 1-334 and a potential hybridizing variant can be determined, for example, by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. *(Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443,1970), as revised by Smith and Waterman (*Adv. Appl. Math* 2:482,1981). The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess (*Nucl. Acids Res.* 14:6745, 1986), as described by Schwartz and Dayhoff (eds., *Atlas of Protein Sequence and Structure,* National Biomedical Research Foundation, pp. 353-358, 1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

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[053] Alternatively, basic protocols for empirically determining hybridization stringency are set forth in section 2.10 of *Current Protocols in Molecular Biology* edited

by F.A. Ausubel et al., John Wiley and Sons, Inc. (1987). Stringency conditions can be determined readily by the skilled artisan. An example of moderate stringency hybridization conditions would be hybridization in 5X SSC, 5X Denhardt's Solution, 50% (w/v) formamide, and 1% SDS at 42°C with washing conditions of 0.2X SSC and 0.1% SDS at 42°C. An example of high stringency conditions can be defined as hybridization conditions as above, and with washing at approximately 68°C, in 0.1X SSC, and 0.1% SDS. The skilled artisan will recognize that the temperature and wash solution salt concentration can be adjusted as necessary according to factors such as the length of the probe.

[054] Due to the degeneracy of the genetic code wherein more than one codon can encode the same amino acid, multiple DNA sequences can code for the same polypeptide. Such variant DNA sequences can result from genetic drift or artificial manipulation (e.g., occurring during PCR amplification or as the product of deliberate mutagenesis of a native sequence). The present invention thus encompasses any nucleic acid capable of encoding a protein derived from SEQ ID NOS: 1-327, or variants thereof.

[055] Deliberate mutagenesis of a native sequence can be carried out using numerous techniques well known in the art. For example, oligonucleotide-directed site-specific mutagenesis procedures can be employed, particularly where it is desired to mutate a gene such that predetermined restriction nucleotides or codons are altered by substitution, deletion or insertion. Exemplary methods of making such alterations are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 12-19, 1985); Smith et al. (*Genetic Engineering: Principles*

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and Methods, Plenum Press, 1981); Kunkel *(Proc. Natl. Acad. Sci. USA* 82:488, 1985); Kunkel et al. (*Methods in Enzymol.* 154:367, 1987); and U.S. Patent Nos. 4,518,584 and 4,737,462, all of which are incorporated by reference.

[056] Thus, the invention further provides an isolated nucleic acid molecule selected from the group comprising of (1), (2), and (3) above and further consisting of:

(4) an isolated nucleic acid molecule degenerate from SEQ ID NOS: 1-334 as a result of the genetic code; and

(5) an isolated nucleic acid molecule selected from the group consisting of an allelic variants and species homologs of SEQ ID NOS: 1-334.

Obtaining Full Length cDNAs

[057] The cDNAs isolated and cloned through the differential display procedure will often only represent a partial sequence (generally the 3' end) of the mRNA from which it was derived due to the nature of the arbitrary primer used in the differential display PCR reaction. Consequently, the cDNA sequences of SEQ ID NOS: 1-327 provide powerful tools for obtaining the sequences of full-length cDNAs. This can be accomplished by using a partial cDNA as a probe to identify and isolate the full length cDNA from a population of full length cDNAs or from a full length cDNA library. As is well known in the art, similar procedures can be used to identify corresponding genomic DNA sequences.

[058] Alternatively, one can obtain the 5' sequence of a partial cDNA by performing Rapid Amplification of cDNA Ends (RACE) procedures such as those disclosed in Frohman, *Methods in Enzymology*, 218:340-356 (1993) and Bertling et al., *PCR Methods and Applications* 3:95-99 (1993) which are hereby incorporated by

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reference. For example, Clonetech Laboratories, Inc. (Palo Alto, CA) offers a SMART™ cDNA product line that allows one to generate high quality full length cDNAs and cDNA libraries. SMART™ technology can also be used to perform RACE. One skilled in the art will readily recognize that there are other equivalent products and procedures for obtaining full length cDNAs. Full length cDNAs may be sequenced and their sequences compared to sequences in public databases to assess their identities and/or homologies to other known sequences.

[059] Cloned full length cDNAs can be used in the construction of expression vectors for the production and purification of pine tree polypeptides which contain the pine tree peptides encoded by the cDNAs of any one of SEQ ID NOS: 1-327.

[060] *Oligonucleotide Primers for PCR Assays*

[061] In another embodiment, the present invention encompasses oligonucleotide fragments derived from any one of SEQ ID NO: 1 through SEQ ID NO: 327 or from the reverse complement sequence of any one of SEQ ID NO: 1 through SEQ ID NO: 327. Such oligonucleotides would be useful as primers in the performance of RT-PCR assays to detect, or even quantify, pine embryo stage-specific transcripts. Such oligonucleotide primers will generally comprise from 10 to 25 nucleotides substantially complementary to the ends of the target sequence and may contain additional non-complementary nucleotides, for example, nucleotides that generate a restriction endonuclease site or cloning junction. Programs useful in selecting PCR primers may be used to design the oligonucleotides of this invention, but use of such programs is not necessary. By way of example, the Wisconsin Package™ software available from the Genetic Computer Group (Madison, Wisconsin) includes a program

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called Prime that can aid in selecting primers from a given template sequence. Protocols for the design and optimization of PCR reactions are commonly known in the art and are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189-196; and PCR Protocols: *A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc. (1990).

Antisense Nucleic Acid Molecules

[062] Other useful fragments of the nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of DNA from any one of SEQ ID NO: 1 through SEQ ID NO: 327. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to about 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*Bio/Techniques* 6:958, 1988).

[063] Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes or other nucleic acid complexes inimical to efficient production of gene products. The antisense oligonucleotides thus may be used to block expression of proteins or the function of RNA. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in

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WO91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sufficient sequence specificity to be able to bind to target nucleotide sequences.

[064] Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10448, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides. Such modifications may modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[065] Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, lipofection, $CaPO^4$-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus or adenovirus.

[066] Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. In one embodiment, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand

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binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[067] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Polypeptides Encoded by Differentially-Expressed cDNAs

[068] The cDNAs of SEQ ID NOS: 1-327 can be translated into amino acid sequences potentially corresponding to portions of developmentally-regulated plant proteins. These amino acid sequences can be identified from sequences listed in Table I, below. The cDNAs encoding these predicted polypeptides are grouped into early, middle, and late transcripts according to the staged embryo population from which they were derived.

(See Table I)

[069] Although the term "peptide" is generally understood to reference synthetic sequences, or fragments of larger proteins, and includes short amino acid sequences of between 2 and 10 amino acids, whereas "polypeptide" refers to larger sequences and full-length proteins, the terms are used interchangeably herein to indicate that the invention applies to peptides and polypeptides of any length and variants thereof. Moreover, the discovery of presumptive open reading frames in SEQ ID NOS: 1-327, and the ability to isolate additional cDNA sequence, enables the construction of expression vectors comprising nucleic acid sequences encoding those polypeptides.

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The cDNAs of the invention also enable cells transfected or transformed with expression vectors driving the expression of the encoded polypeptides and antibodies reactive with the polypeptides.

[070] In one embodiment, the invention provides for isolated polypeptides, preferably, pine tree polypeptides. As used herein, the term "polypeptides" refers to a genus of polypeptide or peptide fragments that encompass the amino acid sequences identified from Table I, as well as smaller fragments. Consequently, the invention encompasses any polypeptide fragment comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids encoded by the cDNAs of any of SEQ ID NOS: 1-327, or comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids of any of amino acid sequence derived from Table I.

[071] Alternatively, a polypeptide may be defined in terms of its antigenic relatedness to any peptide encoded by SEQ ID NOS: 1-327. Thus, in one embodiment, a polypeptide within the scope of the invention is defined as an amino acid sequence comprising a linear or 3-dimensional epitope shared with any peptide encoded by the cDNAs of SEQ ID NOS: 1-327. Alternatively, a polypeptide within the scope of the invention is recognized by an antibody that specifically recognizes any peptide encoded by SEQ ID NOS: 1-327. Antibodies are defined to be specifically binding if they bind pine tree polypeptides with a K_a of greater than or equal to about 10^7 M^{-1}, and preferably greater than or equal to 10^8 M^{-1}.

[072] A polypeptide "variant" as referred to herein means a polypeptide substantially homologous to a native polypeptide, but which has an amino acid sequence different from that encoded by any of SEQ ID NOS: 1-327 because of one or

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more deletions, insertions or substitutions. The variant amino acid sequence preferably is at least 80% identical to a native polypeptide amino acid sequence, preferably at least 90%, more preferably, at least 95% identical over at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21-25, or 26-30 contiguous amino acids. The percent identity between an amino acid sequence encoded by any of SEQ ID NOS: 1-327 and a potential variant can be determined manually, or, for example, by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program, described above, utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443,1970), as revised by Smith and Waterman (*Adv. Appl. Math* 2:482,1981).

[073] Variants can comprise conservatively substituted sequences, meaning that a given amino acid residue is replaced by a residue having similar physiochemical characteristics. Examples of conservative substitutions include substitution of one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. See Zubay, Biochemistry, Addison-Wesley Pub. Co., (1983) incorporated by reference in its entirety. The effects of such substitutions can be calculated using substitution score matrices such a PAM-120, PAM-200, and PAM-250 as discussed in Altschul, (*J. Mol. Bi*ol. 219:555-65, 1991). Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are well known.

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[074] Naturally-occurring peptide variants are also encompassed by the invention. Examples of such variants are proteins that result from alternate mRNA splicing events or from proteolytic cleavage of the polypeptides of Table I. Variations attributable to proteolysis include, for example, differences in the N- or C-termini upon expression in different types of host cells, due to proteolytic removal of one or more terminal amino acids from the polypeptides encoded by the sequences of Table I (generally from 1-5 terminal amino acids).

[075] As stated above, the invention provides recombinant and non-recombinant, isolated and purified polypeptides, preferably pine tree polypeptides. Variants and derivatives of native polypeptides can be obtained by isolating naturally-occurring variants, or the nucleotide sequence of variants, of other plant lines or species, or by artificially programming mutations of nucleotide sequences coding for native pine tree polypeptides. Alterations of the native amino acid sequence can be accomplished by any of a number of conventional methods. Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion. Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene wherein predetermined codons can be altered by substitution, deletion or insertion. Exemplary methods of making such alterations are discussed supra.

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[076] The following sections are examples of the various expression vectors, host cells, and protein purification methods that are known in the art. These examples are provided merely as illustrative and should not be construed as the only means to express and purify the polypeptides and polypeptide variants of the invention.

Expression Vectors and Purified proteins

[077] Recombinant expression vectors containing a nucleic acid sequence encoding the polypeptides of the invention can be prepared using well known methods. In one embodiment, the expression vectors include a cDNA sequence encoding the polypeptide operably linked to suitable transcriptional or translational regulatory nucleotide sequences, such as those derived from a mammalian, microbial, viral, or insect gene. Examples of regulatory sequences include transcriptional promoters, operators, or enhancers, mRNA ribosomal binding sites, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are "operably linked" when the regulatory sequence functionally relates to the cDNA sequence of the invention. Thus, a promoter nucleotide sequence is operably linked to a cDNA sequence if the promoter nucleotide sequence controls the transcription of the cDNA sequence. The ability to replicate in the desired host cells, usually conferred by an origin of replication, and a selection gene by which transformants are identified can additionally be incorporated into the expression vector.

[078] In addition, sequences encoding appropriate signal peptides that are not naturally associated with the polypeptides of the invention can be incorporated into expression vectors. For example, a DNA sequence for a signal peptide (secretory leader) can be fused in-frame to the pine tree nucleotide sequence so that the

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polypeptides of the invention is initially translated as a fusion protein comprising the signal peptide. A signal peptide that is functional in the intended host cells enhances extracellular secretion of the expressed polypeptide. The signal peptide can be cleaved from the polypeptide upon secretion from the cell.

[079] Fusions of additional peptide sequences at the amino and carboxyl terminal ends of the polypeptides of the invention can be used to enhance expression of the polypeptides or aid in the purification of the protein. Such peptides include, for example, poly-His or the antigenic identification peptides described in U.S. Patent No. 5,011,912 and in Hopp et al., (*Bio/Technology* 6:1204, 1988).

[080] Suitable host cells for expression of polypeptides of the invention include prokaryotes, yeast or higher eukaryotic cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described, for example, in Pouwels et al., *Cloning Vectors: A Laboratory Manual*, Elsevier, New York, (1985). Cell-free translation systems could also be employed to the disclosed polypeptides using RNAs derived from DNA constructs disclosed herein.

Prokaryotic expression systems

[081] Prokaryotes include gram negative or gram positive organisms, for example, *E. coli* or *Bacilli*. Suitable prokaryotic host cells for transformation include, for example, *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various other species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. In a prokaryotic host cell, such as *E. coli*, the disclosed polypeptides can include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the

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prokaryotic host cell. The N-terminal methionine can be cleaved from the expressed recombinant polypeptide.

[082] Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. To construct an expression vector using pBR322, an appropriate promoter and a DNA sequence encoding one or more of the polypeptides of the invention are inserted into the pBR322 vector. Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM-1 (Promega Biotec, Madison, WI, USA). Other commercially available vectors include those that are specifically designed for the expression of proteins; these would include pMAL-p2 and pMAL-c2 vectors that are used for the expression of proteins fused to maltose binding protein (New England Biolabs, Beverly, MA, USA).

[083] Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase (penicillinase), lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EP-A-36776), and tac promoter (Maniatis, *MoLecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful prokaryotic host cell expression

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system employs a phage λ P_L promoter and a cI857ts thermolabile repressor sequence. Plasmid vectors available from the American Type Culture Collection ("ATCC"), which incorporate derivatives of the PL promoter, include plasmid pHUB2 (resident in *E. coli* strain JMB9 (ATCC 37092)) and pPLc28 (resident in *E. coli* RR1 (ATCC 53082)).

[084] DNA encoding one or more of the polypeptides of the invention may be cloned in-frame into the multiple cloning site of an ordinary bacterial expression vector. Ideally the vector would contain an inducible promoter upstream of the cloning site, such that addition of an inducer leads to high-level production of the recombinant protein at a time of the investigator's choosing. For some proteins, expression levels may be boosted by incorporation of codons encoding a fusion partner (such as hexahistidine) between the promoter and the gene of interest. The resulting "expression plasmid" may be propagated in a variety of strains of *E. coli*.

[085] For expression of the recombinant protein, the bacterial cells are propagated in growth medium until reaching a pre-determined optical density. Expression of the recombinant protein is then induced, e.g., by addition of IPTG (isopropyl-b-D-thiogalactopyranoside), which activates expression of proteins from plasmids containing a lac operator/promoter. After induction (typically for 1-4 hours), the cells are harvested by pelleting in a centrifuge, e.g., at 5,000 x G for 20 minutes at 4°C.

[086] For recovery of the expressed protein, the pelleted cells may be resuspended in ten volumes of 50 mM Tris-HCl (pH 8)/1 M NaCl and then passed two or three times through a French press. Most highly expressed recombinant proteins forms insoluble aggregates known as inclusion bodies. Inclusion bodies can be purified

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away from the soluble proteins by pelleting in a centrifuge at 5,000 x G for 20 minutes, 4°C. The inclusion body pellet is washed with 50 mM Tris-HCl (pH 8)/1% Triton X-100 and then dissolved in 50 mM Tris-HCl (pH 8)/8 M urea/0.1 M DTT. Any material that cannot be dissolved in 50 mM Tris-HCl (pH 8)/8 M urea/0.1 M DTT may be removed by centrifugation (10,000 x G for 20 minutes, 20°C). The protein of interest will, in most cases, be the most abundant protein in the resulting clarified supernatant. This protein may be "refolded" into the active conformation by dialysis against 50 mM Tris-HCl (pH 8)/5 mM $CaCl_2$ /5 mM $Zn(OAc)_2$/1 mM GSSG/0.1 mM GSH. After refolding, purification can be carried out by a variety of chromatographic methods such as ion exchange or gel filtration. In some protocols, initial purification may be carried out before refolding. As an example, hexahistidine-tagged fusion proteins may be partially purified on immobilized Nickel.

[087] While the preceding purification and refolding procedure assumes that the protein is best recovered from inclusion bodies, those skilled in the art of protein purification will appreciate that many recombinant proteins are best purified out of the soluble fraction of cell lysates. In these cases, refolding is often not required, and purification by standard chromatographic methods can be carried out directly.

Yeast Expression Systems

[088] Polypeptides of the invention can also be expressed in yeast host cells, preferably from the *Saccharomyces* genus (e.g., *S. cerevisiae*). Other genera of yeast, such as *Pichia* or *Kluyveromyces* (e.g. *K. lactis*), can also be employed. Yeast vectors will often contain an origin of replication sequence from a 2μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for

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polyadenylation, sequences for transcription termination, and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionine, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980), or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Hitzeman, EPA-73,657 or in Fleer et. al., *Gene*, 107:285-195 (1991); and van den Berg et. al., *Bio/Technology*, 8:135-139 (1990). Another alternative is the glucose-repressible ADH2 promoter described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). Shuttle vectors replicable in both yeast and *E. coli* can be constructed by inserting DNA sequences from pBR322 for selection and replication in *E. coli* (Amp^r gene and origin of replication) into the above-described yeast vectors.

[089] The yeast α-factor leader sequence can be employed to direct secretion of one or more of the disclosed polypeptides. The α-factor leader sequence is often inserted between the promoter sequence and the structural gene sequence. See, e.g., Kurjan et al., *Cell* 30:933, 1982; Bitter et al., *Proc. Natl. Acad. Sci.* USA 81:5330, 1984; U.S. Patent 4,546,082; and EP 324,274. Other leader sequences suitable for facilitating secretion of recombinant polypeptides from yeast hosts are known to those of skill in the art. A leader sequence can be modified near its 3' end to contain one or more restriction sites. This will facilitate fusion of the leader sequence to the structural gene.

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[090] Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen et al., *Proc. Natl. Acad. Sci.* USA 75:1929, 1978. The Hinnen et al. protocol selects for Trp+ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 µg/ml adenine, and 20 µg/ml uracil.

[091] Yeast host cells transformed by vectors containing ADH2 promoter sequence can be grown for inducing expression in a "rich" medium. An example of a rich medium is one consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 µg/ml adenine and 80 µg/ml uracil. Derepression of the ADH2 promoter occurs when glucose is exhausted from the medium.

Mammalian Expression Systems

[092] Mammalian or insect host cell culture systems could also be employed to express recombinant polypeptides of the invention. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988). Established cell lines of mammalian origin also can be employed. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., *Cell* 23:175, 1981), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, and BHK (ATCC CRL 10) cell lines, and the CV-1/EBNA-1 cell line (ATCC CRL 10478) derived from the African green monkey kidney cell line CVI (ATCC CCL 70) as described by McMahan et al. (*EMBO J.* 10: 2821,1991).

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WASHINGTON, DC 20005
202-408-4000

[093] Established methods for introducing DNA into mammalian cells have been described (Kaufman, R.J., *Large Scale Mammalian Cell Culture*, 1990, pp. 15-69).

Additional protocols using commercially available reagents, such as Lipofectamine (Gibco/BRL) or Lipofectamine-Plus, can be used to transfect cells (Felgner et al., *Proc. Natl. Acad. Sci.* USA 84:7413-7417, 1987). In addition, electroporation can be used to transfect mammalian cells using conventional procedures, such as those in Sambrook et al. Molecular Cloning: A Laboratory Manual, 2 ed. Vol. 1-3, Cold Spring Harbor Laboratory Press, 1989). Selection of stable transformants can be performed using resistance to cytotoxic drugs as a selection method. Kaufman et al., *Meth. in Enzymology* 185:487-511, 1990, describes several selection schemes, such as dihydrofolate reductase (DHFR) resistance. A suitable host strain for DHFR selection can be CHO strain DX-B11, which is deficient in DHFR (Urlaub and Chasin, *Proc. Natl. Acad. Sci.* USA 77:4216-4220, 1980). A plasmid expressing the DHFR cDNA can be introduced into strain DX-B11, and only cells that contain the plasmid can grow in the appropriate selective media. Other examples of selectable markers that can be incorporated into an expression vector include cDNAs conferring resistance to antibiotcs, such as G418 and hygromycin B. Cells harboring the vector can be selected on the basis of resistance to these compounds.

[094] Transcriptional and translational control sequences for mammalian host cell expression vectors can be excised from viral genomes. Commonly used promoter sequences and enhancer sequences are derived from polyoma virus, adenovirus 2, simian virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and later promoter, enhancer, splice, and polyadenylation sites can be used to provide other genetic elements for expression of a structural gene sequence in a mammalian host cell. Viral early and late

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202-408-4000

promoters are particularly useful because both are easily obtained from a viral genome as a fragment, which can also contain a viral origin of replication (Fiers et al., *Nature* 273:113, 1978; Kaufman, *Meth. in Enzymology*, 1990). Smaller or larger SV40 fragments can also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* I site located in the SV40 viral origin of replication site is included.

[095] Additional control sequences shown to improve expression of heterologous genes from mammalian expression vectors include such elements as the expression augmenting sequence element (EASE) derived from CHO cells (Morris et al., *Animal Cell Technology*, 1997, pp. 529-534) and the tripartite leader (TPL) and VA gene RNAs from Adenovirus 2 (Gingeras et al., *J. Biol. Chem.* 257:13475-13491, 1982). The internal ribosome entry site (IRES) sequences of viral origin allows dicistronic mRNAs to be translated efficiently (Oh and Sarnow, *Current Opinion in Genetics and Development* 3:295-300, 1993; Ramesh et al., *Nucleic Acids Research* 24:2697-2700, 1996). Expression of a heterologous cDNA as part of a dicistronic mRNA followed by the gene for a selectable marker (eg. DHFR) has been shown to improve transfectability of the host and expression of the heterologous cDNA (Kaufman, *Meth. in Enzymology*, 1990). Exemplary expression vectors that employ dicistronic mRNAs are pTR-DC/GFP described by Mosser et al., *Biotechniques* 22:150-161, 1997, and p2A5I described by Morris et al., *Animal Cell Technology*, 1997, pp. 529-534.

[096] A useful high expression vector, pCAVNOT, has been described by Mosley et al., Cell 59:335-348, 1989. Other expression vectors for use in mammalian host cells can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280,

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202-408-4000

1983). A useful system for stable high level expression of mammalian cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986). A useful high expression vector, PMLSV N1/N4, described by Cosman et al., *Nature* 312:768,1984, has been deposited as ATCC 39890. Additional useful mammalian expression vectors are described in EP-A-0367566, and in U.S. Patent Application Serial No. 07/701,415, filed May 16, 1991, incorporated by reference herein. The vectors can be derived from retroviruses. In place of the native signal sequence, a heterologous signal sequence can be added, such as the signal sequence for IL-7 described in United States Patent 4,965,195; the signal sequence for IL-2 receptor described in Cosman et al., Nature 312:768 (1984); the IL-4 signal peptide described in EP 367,566; the type I IL-1 receptor signal peptide described in U.S. Patent 4,968,607; and the type H IL-1 receptor signal peptide described in EP 460,846.

[097] The polypeptides of the invention and the nucleic acid molecules encoding them can also be used as reagents to identify (a) proteins that the disclosed polypeptides or their constituent proteins regulate, and (b) other proteins with which it might interact. The disclosed polypeptides can be coupled to a recombinant protein, to an affinity matrix, or by using them as a bait in the yeast two-hybrid system. The use of the yeast two-hybrid system developed by Stanley Fields and coworkers is well known in the art and described in Golemis, E., et al Section 20.1 in: Current Protocols in Molecular Biology, ed. Ausubel, F.M., et al., John Wiley & Sons, NY, 1997 and in *The Yeast Two-Hybrid System.*, ed. P.L. Bartel and S. Fields, Oxford University Press, 1997.

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Antibodies and Peptide Binding Proteins

[098] Purified polypeptides of the invention can be used to generate antibodies that bind to one or more epitopes of the disclosed polypeptide. Such anti-polypeptide antibodies includes polyclonal antibodies, monoclonal antibodies, fragments thereof such as F(ab')2, and Fab fragments, as well as any recombinantly produced binding partners. Antibodies are defined to be specifically binding if they bind pine tree polypeptides with a K_a of greater than or equal to about 10^7 M^{-1}. Affinities of binding partners or antibodies can be readily determined using conventional techniques, for example, those described by Scatchard et al., *Ann. N.Y. Acad. Sci.*, 51:660 (1949).

[099] Polyclonal antibodies can be readily generated from a variety of sources, for example, horses, cows, goats, sheep, dogs, chickens, rabbits, mice, hamsters, guinea pigs, or rats, using procedures that are well-known in the art, for example, as described for example, in U.S. Patent 5,585,100, incorporated by reference herein. In general, a composition comprising at least one of the polypeptides of the invention is administered to the host animal, typically through intra-peritoneal or subcutaneous injection. In the case where a peptide is used as the immunogen, it is preferable to conjugated it to a suitable carrier molecule, such as a T-dependent antigen (Bovine Serum Albumin, cholera toxin, and the like). The immunogenicity of the disclosed polypeptides can also be enhanced through the use of an adjuvant, for example, Freund's complete or incomplete adjuvant or alum. Following booster immunizations, small samples of serum are collected and tested for reactivity to the disclosed polypeptides or their constituent epitopes. Examples of various assays useful for such determination include those described in: *Antibodies: A Laboratory Manual*, Harlow and

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1300 I STREET, N. W.
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Lane (eds.), Cold Spring Harbor Laboratory Press, 1988; as well as procedures such as countercurrent immuno-electrophoresis (CIEP), radioimmunoassay, radio-immunoprecipitation, enzyme-linked immuno-sorbent assays (ELISA), dot blot assays, and sandwich assays, see U.S. Patent Nos. 4,376,110 and 4,486,530, each of which is incorporated by reference in their entirety.

[0100] Monoclonal antibodies (or fragments thereof), directed against epitopes of the disclosed polypeptides can also be readily prepared using well-known procedures, such as, for example, the procedures described in U.S. Patent Nos. RE 32,011, 4,902,614, 4,543,439, and 4,411,993; *Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses*, Plenum Press, Kennett, McKearn, and Bechtol (eds.), 1980, each of which is incorporated by reference. Briefly, the host animals, such as mice, are injected intraperitoneally at least once, and preferably at least twice at about 3 week intervals with isolated and purified polypeptides optionally in the presence of adjuvant. Again, if peptide fragments are used they may need to be conjugated to a suitable carrier protein. Mouse sera are then assayed by conventional dot blot technique or antibody capture (ABC) to determine which animal is best to fuse. Approximately two to three weeks later, the mice are given an intravenous boost of pine tree polypeptides. Mice are later sacrificed and spleen cells fused with commercially available myeloma cells, such as Ag8.653 (ATCC), following established protocols. Briefly, the myeloma cells are washed several times in media and fused to mouse spleen cells at a ratio of about three spleen cells to one myeloma cell. The fusing agent can be any suitable agent used in the art, for example, polyethylene glycol (PEG). Fusion is plated out into plates containing media that allows for the selective growth of

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202-408-4000

the fused cells. The fused cells can then be allowed to grow for approximately eight days. Supernatants from resultant hybridomas are collected and added to a plate that is first coated with goat anti-mouse Ig. Following washes, a label, such as, ^{125}I- pine tree polypeptides is added to each well followed by incubation. Positive wells can be subsequently detected by autoradiography. Positive clones can be grown in bulk culture and supernatants are subsequently purified over a Protein A column (Pharmacia).

[0101] Monoclonal antibodies and specific-binding fragments of the invention can be produced using alternative techniques, such as those described by Alting-Mees et al., "Monoclonal Antibody Expression Libraries: A Rapid Alternative to Hybridomas", *Strategies in Molecular Biology* 3:1-9 (1990), which is incorporated herein by reference. Similarly, binding partners can be constructed using recombinant DNA techniques to incorporate the variable regions of a gene that encodes a specific binding antibody. Such a technique is described in Larrick et al., *Biotechnology*, 7:394 (1989).

[0102] It is understood of course that many techniques could be used to generate antibodies against the polypeptides of the invention and that the above embodiments in no way limits the scope of the invention.

Nucleotides, Proteins, Antibodies, and Binding Proteins As Probes and Reagents

[0103] The disclosed nucleic acids, polypeptides, and antibodies directed against the disclosed polypeptides can be used in a variety of research protocols, such as in DNA arrays or as reagents. A sample of such research protocols are given in Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1-3, Cold Spring Harbor Laboratory Press, (1989), incorporated by reference. For example, the compiled

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sequences, polypeptides, etc., can serve as markers for cell specific or tissue specific expression of RNA or proteins. Similarly, this system can be used to investigate constitutive and transient expression of the genes encoding the cDNAs of SEQ ID NOS: 1-327 and the proteins encoded by these genes.

[0104] Further, the disclosed cDNA sequences can be used to determine the chromosomal location of the genomic DNA and to map genes in relation to this chromosomal location. The disclosed nucleotide sequence can be further used to identify additional genes related to the nucleotides of SEQ ID NOS: 1-334 and to establish evolutionary relatedness among species based on the comparison of sequences. The disclosed nucleotide and polypeptide sequences can be used to select for those genes or proteins that are homologous to the disclosed cDNAs or polypeptides, using well-established positive screening procedures such as Southern blotting and immunoblotting and negative screening procedures such as subtractive hybridization.

Method for Using Nucleic Acid Probes or Antibodies to Stage Embryos

[0105] Accurate staging of tree embryos is critical. It is known that different stages of tree embryos have different capacities as subjects for genetic transformation and genetic engineering. In addition, environmental requirements exhibited by embryos vary due to increasing physiologic age. Currently, the staging of tree embryogenesis is most accurately performed by an expert in the field who is very familiar with the morphological appearance of embryos at different stages. The cDNAs and related molecules of this invention can be used as markers for different stages of tree embryogenesis, thereby eliminating the need for a subjective eye to assess maturity

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and potentially allowing for more accurate staging of tree embryos. Moreover, by monitoring the expression of the underlying genes, it is possible to determine when an embryo has reached a certain level of development even if that level does not correspond to a visible difference in embryo morphology. The relational database of this invention aids the ability to monitor expression levels and tailor research approaches, such as the use of DNA arrays, to the specific needs of the objective, i.e., staging.

[0106] The information provided in this invention can be used in whole or in part to stage embryos. For example, one or a multiplicity of nucleic acid molecules from SEQ ID NOS: 1-327 having an expression profile consistent with a particular embryo stage can be used in this invention. A researcher may find it beneficial to use oligonucleotide probes or antibodies, for example, that specifically recognize proteins derived from genes expressed during middle embryonic stages, or that specifically monitor expression levels for embryos that have reached maturity associated with late developmental stages. A researcher can quickly determine that an embryo subset has progressed to or through an embryonic stage with the use of this invention and make appropriate changes in conditions if necessary, e.g. alter growth media or other environmental conditions.

Method for Monitoring, Enhancing, or Determining Expression of Stage-Specific Genes

[0107] Expression patterns of SEQ ID NOS: 1-327 indicate that gene activation can be classified as stage-specific, such as in the case of SEQ ID NO: 327, otherwise known as "LP2-3." The promoter that drives such a gene can perform valuable functions. For example, a promoter from LP2-3 operatively linked to a reporter gene presented within an embryo system is expected to produce the reporter product under

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202-408-4000

the conditions for expression of gene LP2-3. Thus, the system allows a rapid determination of stage specific embryos by a simple phenotypic reporter screen, perhaps by visualization of green fluorescent protein (GFP) or by loss of fluorescent protein product. Similarly, a set of promoters from known, differently staged genes operatively linked to reporter genes will be effective for monitoring developmental changes within the system as the embryos mature. The LP2-3 promoter is identified as SEQ ID NOS: 328-334 in Table I. The promoter expression pattern is that of the natively linked gene, LP2-3.

[0108] Virtually any indicator or reporter gene can be used for this approach or for other methods associated with this invention provided they are compatible with the system studied. Generally, reporter genes are genes typically not present in the recipient organism or tissue and which encode for proteins resulting in some phenotypic change or enzymatic property. Examples of such genes and assays are provided by Schenborn, E. and Groskreutz, D., Mol. Biotechnol., 13:29, 1999; Helfand, S. L. and Rogina, B., Results Probl. Cell Differ., 29:67, 2000; Kricka, L.J., Methods Enzymol., 305:333, 2000; Himes, S.R. and Shannon, M. F., Methods Mol. Biol., 130:165, 2000; and Leffel, S. M. et al., Biotechniques, 23:912, 1997, which are incorporated in their entirety by reference. In one embodiment of this invention, the reporter used is GFP, or any ariant of the fluorescent protein.

[0109] Additionally, one skilled in the art would recognize that a promoter, like that from LP2-3, has potential to stimulate production of products not ordinarily observed at a particular stage. A promoter derived from a gene that expresses during a known stage, for example an early stage, can be operatively linked to a gene that does

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not normally express during that stage, yielding controlled expression of any targeted gene. It may be shown that earlier or later expression, or prolonged expression of a particular gene may give a desirable genotype or phenotype in a mature plant, may result in increased vigor in culture, or may be sufficient to alter the normal maturation process of the embryo. Prolonged expression of any desired gene also may be achieved from linking a constitutively expressed promoter to the targeted gene. Further, the ability to manipulate gene expression during embryogenesis allows for a detailed study of the effects of an individual gene or multiple genes on embryogenesis, leading to a better understanding of the developmental processes involved in embryogenesis.

Method of Correlating Gene Expression with Improved Tree Stock or Culture Conditions

[0110] Importantly, the cDNAs and related molecules of the invention can also be used as markers to examine genetic heterogeneity and heredity through the use of techniques such as genetic fingerprinting. These markers can also be correlated with improved agronomic traits including good initiation frequency, embryonic maturation, high frequency of germination, rapid growth rates, herbicide tolerance, insect resistance, pathogen resistance, climate and environmental adaptability wood quality, and wood fiber quality and content, to name a few. Additionally, the expression of these developmentally regulated genes can be compared among genetically identical clones grown under different culture conditions to determine the best protocols and media for somatic embryogenesis.

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[0111] Cryogenic storage of pine tree embryos is effective for maintaining stocks of embryos determined by this invention to have the desired fitness traits or exist at the

appropriate developmental stage. With such storage, one can specifically target desirable embryos for expansion many years after they are frozen. For example, a culture of somatic embryos can be divided into at least three portions, one of which is cryogenically stored, one which is used to study gene embryonic gene (and protein) expression, and one that is used to produce seedlings for field testing. Clones producing valuable mature plants could be selected and expanded from frozen stocks. Additional clones exhibiting similar expression patterns could be selected for future expansion and cultivation.

[0112] As will be evident to the ordinary practitioner, there are numerous ways in which the nucleic acids, polypeptides and antibodies of this invention might be used to characterize the gene expression of embryos. Ideally the stage-specific gene expression of embryos of several different genotypes and at several different stages of embryogenesis are characterized. For example, sets of oligonucleotide primers designed using any one of SEQ ID NOS: 1-327 may be used in RT-PCR assays to characterize expression of a gene product. *In situ* hybridization assays or antibody staining protocols may also be used to characterize RNA and/or protein expression and localization.

[0113] Embryos of the same genotype in which gene expression has been characterized may also used be to generate plantlets that are used in field testing. Once the embryos have developed into mature trees, the various genotype trees can be evaluated for important traits such as growth rates, herbicide tolerance, insect resistance, pathogen resistance, climate and environmental adaptability, wood quality, and wood fiber quality and content, among others. Finally the phenotypic data collected

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202-408-4000

from the field testing can be correlated with gene expression during early embryogenesis to further enhance the database of the present invention. This will allow further identification of gene products which whose expression is correlated, either positively or negatively, with commercially valuable tree characteristics.

[0114] It will be clear to those skilled in the art that identification of such gene products can have several uses. Determining the correlation between a desirable phenotype and a genotype would allow for the "pre-selection" of tree embryos for field testing. It would also be useful in evaluating experimental tissue culture conditions for somatic embryogenesis; in other words, the expression level of a gene known to correlate with the development of trees with desirable characteristics could serve as the criterion on which culture media is evaluated, as opposed to assessing the phenotype of fully matured trees. The ability to evaluate culture conditions without having to develop fully mature trees and do field testing would save a great deal of research time and expense. And of course, the knowledge of the correlation between gene expression and desirable tree phenotypes would serve to identify target genes for genetic engineering.

Genetically Engineering Trees and Other Plants

[0115] There are several methods known in the art for the creation of transgenic plants. These include, but are not limited to: electroporation of plant protoplasts, liposome-mediated transformation, polyethylene-glycol-mediated transformation, microinjection of plant cells, and transformation using viruses. Because the invention is especially concerned with the transformation of woody species, the two prevalent methods for transforming forest trees, namely *Agrobacterium*-mediated transfer and

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WASHINGTON, DC 20005
202-408-4000

direct gene transfer by particle bombardment, will be discussed in more detail, though it is understood that the present invention encompasses generation of transgenic plants via standard methods commonly known in the art.

Agrobacterium Mediated Transfer

[0116] *A. tumefaciens* and *A. rhizogenes* are two soil microorganisms that naturally infect a wide variety of plants including dicotyledonous plants, gymnosperms and some monocotyledonous plants. Infection by these organisms results in the growth of crown gall tumors or in hairy root disease, respectively. Each of these organisms carries a large plasmid, the tumor inducing (Ti) plasmid, in the case of *A. tumefaciens* and the root-inducing (Ri) plasmid in the case of *A. rhizogenes*. These plasmids have two critical features, a set of virulence genes and a segment of DNA called T-DNA that is delimited by conserved regions of approximately 25 base pairs known as the left and right borders. During infection, the T-DNA is transferred to the plant cell where it is able to stably integrate in single copy in the plant genome. Transfer of T-DNA requires the function of the virulence genes.

[0117] In its natural state, T-DNA contains genes that mediate progression of disease such as growth hormones or genes controlling root morphogenesis. Using recombinant DNA technology, however, T-DNA may be modified to contain an expression cassette encoding a foreign gene of interest. There are several T-DNA vector systems commonly in use for the transformation of plants. Several of these vector systems are reviewed in Hansen et al., *Current Topics in Microbiology and Immunology* 240: 21-57 (1999) which is hereby incorporated by reference. T-DNA vectors must include the left and right borders. In addition they must either be capable

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202-408-4000

of replication in *Agrobacterium* or be designed so as to recombine with a plasmid that does so. The latter type of vector is known as a co-integrate vector. For transformation to proceed, there must also be a source of virulence (*vir*) genes. The *vir* genes may be on the same plasmid with the T-DNA or more likely supplied by a helper plasmid. For example, binary T-DNA vector systems are comprised of two plasmids, one containing the vir genes and the other containing T-DNA. Some plants known to be recalcitrant to Agrobacterium-mediated transformation may be transformed if additional copies of some or all virulence genes are provided. Extra copies of VirG and VirE can be particularly useful.

[0118] Additionally, it is convenient to include in the T-DNA a selectable marker that will allow identification and selection of transformed plant cells. The selectable marker should be one that works in both Agrobacterium and the target plant. For example, the genes encoding chloramphenicol acetyltransferase and neomycin phosphotransferase are suitable marker genes that confer resistance to chloramphenicol and kanamycin, respectively. Additionally, a selectable marker may be provided on a separate T-DNA from the T-DNA encoding the gene of interest. Co-transformed T-DNAs can integrate at separate sites in the plant genome. This can be useful because it will later allow segregation of the marker gene in progeny enabling the generation of transgenic trees expressing the gene of interest but not the marker gene.

[0119] The gene of interest and the selectable marker genes must also be under the control of promoters that function in the transformed plant cell. Examples of suitable promoters include, but are not limited to: the abscisic acid (ABA)-inducible promoter

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1300 I STREET, N. W.
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202-408-4000

from the early methionine (*Em*) gene from wheat (Marcotte et al., *Plant Cell* 1:976-979 (1989); the cauliflower mosaic virus (CaMV) 35S promoter (Odell et al., *Nature* 313:810-812 (1985); and the nopaline synthase (nos) promoter (Sanders et al., *Nucl. Acids Res.* 15(4):1543-58 (1987). Tissue-specific plant promoters or plant promoters responsive to chemical, hormone, heat or light treatments may be used. Additionally, the gene of interest may be expressed under the control of its endogenous promoter to ensure proper regulation.

[0120] The process of transformation requires plant cells that are competent and that are either embryogenic or organogenic. The plant cells to be transformed are then co-cultivated with *Agrobacterium* containing an engineered T-DNA vector system for 1-5 days. Following the co-cultivation period, the cells are incubated with the antibiotic against which the selectable marker confers resistance, and transformed lines are selected for further cultivation. The use of *Agrobacterium* mediated transfer in woody trees is described in Loopstra et al., *Plant Molecular Biology* 15:1-9 (1990), Gallardo et al., *Planta* 210:19-26 (1999) and Wenck et al., *Plant Molecular Biology* 39:407-419 (1999), each of which is hereby incorporated by reference.

Direct Gene Transfer by Particle Bombardment

[0121] Direct gene transfer by particle bombardment provides another method for transforming plant tissue. This method can be especially useful when plant species are recalcitrant to transformation by other means. In this technique a particle, or microprojectile, coated with DNA is shot through the physical barriers of the cell. Particle bombardment can be used to introduce DNA into any target tissue that is penetrable by DNA coated particles, but for stable transformation, it is imperative that

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WASHINGTON, DC 20005
202-408-4000

regenerable cells be used. Typically, the particles are made of gold or tungsten. The particles are coated with DNA using either $CaCl^2$ or ethanol precipitation methods which are commonly known in the art.

[0122] DNA coated particles are shot out of a particle gun. A suitable particle gun can be purchased from Bio-Rad Laboratories (Hercules, CA). Particle penetration is controlled by varying parameters such as the intensity of the explosive burst, the size of the particles, or the distance particles must travel to reach the target tissue.

[0123] The DNA used for coating the particles should comprise an expression cassette suitable for driving the expression of the gene of interest. Minimally this will comprise a promoter operably linked to the gene of interest. As with *Agrobacterium* mediated transformation. Suitable promoters include, but are not limted to, the the abscisic acid (ABA)-inducible *Em* promoter from wheat (Marcotte et al., *Plant Cell* 1:976-979 (1989), the CaMV35S promoter (Odell et al., *Nature* 313:810-812 (1985), and the NOS:promoter (Sanders et ., *Nucl. Acids Res.* 15(4):1543-58 (1987).

[0124] Methods for performing direct gene transfer by particle bombardment are disclosed in U.S. Patent 5,990,387 to Tomes et al. Additionally, Ellis et al. describe the successful use of direct gene transfer to white spruce and larch trees in *Bio/Technology* 11, 84-89 (1993).

[0125] Researchers skilled in the area of DNA or gene transformation will recognize that additional procedures, or combination of procedures, may be useful for the successful tranformation of genetic stock.

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& DUNNER, L.L.P.
1300 I STREET, N. W.
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202-408-4000

Antisense Expression

[0126] The cDNAs of the invention may be expressed in such a way as to produce either sense or antisense RNA. Antisense RNA is RNA that has a sequence which is the reverse complement of the mRNA (sense RNA) encoded by a gene. A vector that will drive the expression of antisense RNA is one in which the cDNA is placed in "reverse orientation" with respect to the promoter such that the non-coding strand (rather than the coding strand) is transcribed. The expression of antisense RNA can be used to down-modulate the expression of the protein encoded by the mRNA to which the antisense RNA is complementary. This phenomenon is also known as "antisense suppression." It is believed that down-regulation of protein expression following antisense RNA is caused by the binding of the antisense RNA to the endogenous mRNA molecule to which it is complementary, thereby inhibiting or preventing translation of the endogenous mRNA.

[0127] The antisense RNA expressed need not be the full-length cDNA and need not be exactly homologous to the target mRNA. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous mRNA will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. The length of the antisense sequence in the vector may be greater than 100 nucleotides. Vectors producing antisense RNA's could be used to make transgenic plants, as described above, in situations when desirable tree

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& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

characteristics are produced when the expression of a particular gene is reduced or inhibited.

METHODS

Tissue Samples

[0128] The cDNAs of the current invention can be derived from any sets of plant tissue. The cDNAs of SEQ ID NOS: 1-334, for example, were originally derived from embryonic tissues of pine tree embryos staged 1-9.9 as classified in Pullman and Webb TAPPI R&D Division 1994 Biological Sciences Symposium, pages 31-34, which is hereby incorporated by reference. LPS and LPZ clones are derived from somatic and zygotic embryos, respectively. As noted, embryos may be of either somatic or zygotic derivation, and the embryos may be grown in either semi-solid or liquid tissue culture systems. Applicable methods for growing embryos in semi-solid or liquid tissue culture systems are disclosed in U.S. Patents: 5,036,007; 5,236,841; 5,294,549; 5,413,930; 5,491,090; 5,506,136; 5,563,061; 5,677,185; 5,731,203; 5,731,204; and U.S. Patent Application 60/212,651 filed June 19, 2000, which are hereby incorporated by reference.

RNA Isolation

[0129] In one embodiment, RNA isolated from staged cell populations provides the starting material for reverse transcription, differential display, and cloning of amplified cDNA. Methods and kits for isolating total RNA from cellular populations, or for generating poly(A)+ RNA, are commonly known in the art. For example, several procedures for isolating RNA are disclosed in Chapter 4 of *Current Protocols in Molecular Biology* edited by F.A. Ausubel et al., John Wiley and Sons, Inc. (1987)

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(incorporated herein by reference). As an example, the TRI Reagent7 available from Molecular Research Center, Inc. (Cincinnati, OH) is a suitable reagent (used according to the manufacturer's instructions) for isolation of RNA from plant tissues.

Differential Display

[0130] Differential display provides a method to identify individual messenger RNAs that are differentially expressed among two or more cell populations. In the practice of the present invention, these cell populations may be provided by pine tree or other plant embryos of different developmental stages. The differential display procedure is taught in Liang et al., *Science*, 257:967-71 (1992) and in U.S. Patent No. 5,262,311, which are hereby incorporated by reference. Briefly, mRNA sequences are PCR-amplified using two types of oligonucleotide primers known as "anchor" and "arbitrary" primers. Anchor primers are designed to recognize the polyadenylate tail of messenger RNAs. Arbitrary primers are short and arbitrary in sequence and anneal to complementary sequences in various mRNAs. Products amplified with these primers will vary in size and can be differentiated on an agarose or sequencing gel based on their size. If different cell populations are amplified with the same anchor and arbitrary primers, one can compare the amplification products to identify differentially expressed RNA sequences.

Cloning

[0131] PCR-amplified bands representing differentially expressed RNA samples are excised from the gel, transferred to tubes and reamplified using the same primer pairs and PCR conditions as used in the differential display procedure. Methods for the cloning of PCR products are commonly known in the art and there are several

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commercially available reagents and kits for cloning PCR products. For instance, the pCR-Scipt™ Cloning kit from Stratagene, La Jolla, California) is suitable for this purpose. Using this kit, *E. coli* transformants containing plasmids with PCR fragment inserts can rapidly be identified using blue/white color selection followed by plasmid purification and restriction digests. The pCR-Script vector contains T3 and T7 polymerase recognition sites allowing for in vitro transcription of the inserted fragment.

Sequence Determination

[0132] Methods for sequencing DNA, including cloned PCR products, are commonly known in the art. The selection of cloning vectors having M13, T7 or T3 primer annealing sites flanking the PCR-amplified insert can be used in sequencing reactions directly. Most sequencing procedures in use today are modifications of Sanger's dideoxy chain termination sequencing reaction as disclosed in and Sanger et al., *Proceedings of the National Academy of Sciences*, 74:5463-5467 (1977), which is hereby incorporated by reference.

Homology Searching and Identification of Protein Coding Sequences

[0133] As understood by one of ordinary skill in the art, the sequence of a cloned cDNA insert obtained, may be compared against public databases such as Genbank to discern any identity or homology to known sequences. Programs, such BLAST, for performing such a search are available on the National Center for Biotechnology Information's web page located at http://www.ncbi.nlm.nih.gov. The results from Genbank search may reveal the potential function of a polypeptide or RNA molecule encoded by the cDNA. In addition to searching gene sequence database, the use of commercially available analysis software is well known in the art. For example,

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software packages such as the Wisconsin Package™ (Genetic Computer Group, Madison, Wisconsin) include programs such as FRAMES and CodonPreference that help to identify protein coding sequences in a query nucleotide sequence. FRAMES displays open reading frames for the six DNA translation frames, allowing one to quickly assess the presence or absence of stretches of open-reading frames that are likely to be protein encoding regions. CodonPreference is a more sophisticated program that identifies and displays possible protein coding regions based on similarity of the codon usage in the sequence to a codon frequency table (Gribskov et al., 1984).

EXAMPLE 1: Differential Gene Expression Analysis in Pine Tree Embryogenesis

[0134] cDNA libraries were prepared from staged pine tree embryos, as described above. The differential display technique was used to identify 327 novel cDNAs that were preferentially-expressed during early, middle, or late stages of pine tree embryogenesis, as set forth below. Clone nomenclature is divided into subsets based on tissue type; a clone is designated LPS to indicate somatic origins and LPZ for zygotic origins.

Plant Materials

[0135] Somatic embryos were collected at different stages of development. Cultures of somatic embryos of were initiated from Loblolly pine immature zygotic embryos as described by Becwar et al., *Forestry Science* 44:287-301 (1994) (incorporated by reference) or with minor modifications in media mineral composition. Somatic embryos were grown in cell suspension culture medium 16 (Pullman and Webb, Tappi R&D Division 1994 Biological Sciences Symposium) and a maturation medium similar to that of a standard maturation media. Resulting somatic embryos

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were selected and classified as stages 1-9 according to morphological development following the teachings of Pullman and Webb, Tappi R&D Division 1994 Biological Sciences Symposium pp.31-34. Somatic embryos were sorted into tubes containing the same stages and stored at -70 °C.

RNA Isolation

[0136] Total RNA was isolated from all stages of somatic embryos of loblolly pine and grouped into early, middle, and late phases of development. The early phase is represented by a liquid suspension culture containing embryos of stages 1 through stage 3. Middle phase contains embryos of stages 4 through stage 6, while stages 7 through 9 formed the late phase. 60-100 mg aliquots of staged frozen embryos were ground in 1.0 ml of TRI Reagent® Isolation Reagent (Molecular Research Center, Inc.), a commercial product that includes phenol and guideline thiocyanate in a monophase solution and extracted according to the manufacturer's instructions.

Reverse Transcription of mRNA (RT-PCR)

[0137] The total RNA was used as a template to synthesize single stranded DNA mediated by MMLV reverse transcriptase (100 U/µl). The method involves the reverse transcription by PCR of the mRNA with an oligo-dT primer (H-T_{11}G: 5' B AAGCTTTTTTTTTTTG 3') anchored to the beginning of the poly(A) tail, followed by a PCR reaction in the presence of a second short (13-mer) primer which is arbitrary in sequence [AP_1 (5' B AAGCTTGATTGCC - 3') or AP_2 (5' B AAGCTTCGACTGT - 3')]. Reverse transcription and Differential Display were conducted using the GenHunter RNAimage Kit I.

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[0138] A 19 µl reverse transcription reaction (10 µl sterile water, 2.0 µl 5x RT buffer, 1.6 µl dNTP (250 µM), 2.0 µl anchored primer (2.0 µM), 2.0 µl RNA template at 100 ng/µl) was prepared for each embryo phase sample. The reaction mixture was heated to 65°C for 5 minutes in a thermocycler, cooled to 37°C and paused after 10 minutes while 1.0 µl MMLV was added. The program was allowed to resume at 37°C for 50 minutes. The reaction was then heated to 75°C for 5 minutes, cooled to 4°C and stored at -20°C.

Incorporation of Radiolabeled Nucleotides by PCR

[0139] Differential Display PCR was performed in a 20 µl reaction containing 2 µl of the reverse-transcribed cDNA template; 10 µl sterile water 2.0 µl 10x PCR buffer, 1.6 µl dNTP (25 µM), 2.0 µl anchored primer H-T11 G, (2.0 µM), 2.0 µl 13 mer arbitrary primer (AP_1 or AP_2 (2.0 µM), 0.2 µl Taq DNA polymerase, and 0.2 µl α^{32}P-dATP (2000 Ci/mmole). The cDNA was amplified by PCR: 94°C for 3 minutes, 40 cycles of 94°C for 30 seconds, 40°C for 2 minutes, and 72°C for 30 seconds, followed by 72°C for 5 minutes. The reaction was cooled to 4°C and stored at -20°C.

Differential Display

[0140] The PCR products were separated on a Stratagene (La Jolla, California) pre-cast 6% polyacrylamide sequencing gel at 30 watts constant power for approximately 2.5 to 3 hours. 3.5 µl of sample was mixed with 2.0 µl of loading dye and incubated at 80°C for 2 minutes immediately before loading onto the gel. The gel was rinsed in water and dried. Dilute ^{33}P-dATP with loading dye was spotted at the corners

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as alignment markers and the gels were exposed to Kodak BioMax™ autoradiography film. An exemplary gel is shown in Figure 1.

[0141] Bands that appeared to be possible markers for phase specific gene expression were marked on the film and aligned over the gel. The bands were excised by cutting through the film. The gel pieces were scraped from the gel and transferred to tubes and re-amplified using the same primer pairs and PCR conditions as used for incorporation of radiolabeled nucleotides.

Cloning of DNA Fragments from Differential Display

[0142] The PCR products from the gel fragments were purified, polished, ligated and cloned into XL 10-Gold Kan ultracompetent cells by heat shock with the Stratagene pCR-Script Amp SK(+) Supercompetent Cell Cloning Kit according to manufacturer's instructions. The transformed cells were spread on LB agar plates containing ampicillin, IPTG, and X-Gal each at 50 µg/ml. The plates were incubated overnight at 37°C. Plasmids containing PCR inserts were identified using blue-white colony screening. The presence of inserts was confirmed by digesting the clones with restriction endonucleases, Msc I and Nla III, followed by standard DNA gel electrophoresis. Transformants representing early, middle, and late phase embryos were sequenced using standard dideoxy protocols known in the art with the T3 primer.

Sequence Analysis

[0143] All sequences were analyzed using a program-database pair search of the NCBI BLAST 2.0 server, blastn-nr, blastn-others ests, and blastx-nr. In each case, the query sequence was filtered for low complexity regions by default and entered in FASTA format. Other formatting options were set by default; alignment view-pairwise,

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descriptions-100, and alignments-50. Using these parameter settings, significant similarity to known DNA, RNA, or protein sequences was found for several of the nucleic acid molecules of SEQ ID NOS: 1-334, for example, those described herein. (Alignment data not shown).

EXAMPLE 2: Characterization of Full Length LP2-3 cDNA Sequence

[0144] SEQ ID NO: 327, designated LP2-3, was first identified through differential display with $T_{12}MG$ and AP_1 primers (GeneHunter). The differential display band appeared to be present only in liquid suspension cultures of Loblolly Pine somatic embryos. The conditions for mRNA isolation, reverse-transcription, differential display-PCR, and gel separation/visualization for producing this band were all as described in Example 1. Likewise, the band containing the original LP2-3 fragment was excised from the differential display gel, amplified, and cloned into pCR-Script AMP SK(+) according to standard protocols known in the art.

Northern Hybridizations Demonstrating Early-Specific Expression

[0145] Northern analysis demonstrated that the LP2-3 differential display clone hybridized to an approximately 1.2 Kb mRNA from liquid suspension culture embryos but was undetectable in late (6-9) stage embryo RNA. (Figure 11) In general, LP2-3 is most highly expressed in early stage embryos in liquid culture. LP2-3 mRNA is found most abundantly in early stage somatic embryos, especially for embryos grown in liquid multiplication medium. (Figure 12) Further, transcription decreases rapidly as embryos are transferred to maturation medium (stage 3 and stage 4) and begin to mature. LP2-3 transcripts are virtually undetectable at stage 6-9 somatic embryos grown on maturation medium. (See Figure 12) Additional studies indicate that LP2-3 mRNA is expressed

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zygotically, particularly in early stage zygotic embryos, but is undetectable in mature vegetative tissues. (Figures 13 and 14) Specifically, the signal intensity from liquid suspension somatic embryo RNA was about 3 times greater than the signal from the analogous stage 1 zygotic embryo RNA. (Figures 13 and 14) LP2-3 transcripts were not detectable in total RNA from needles, stems, or roots of one year old seedlings, including those exposed to cold, ozone, wound stresses, or the hormone jasmonic acid (not shown).

LP2-3 Differential Display and 'Full-Length' cDNA Sequences

[0146] A 'full-length' cDNA was captured from SMART™ cDNA made from somatic embryo liquid suspension by using a biotinylated LP2-3 differential display fragment as a capture probe. The "full-length" cDNA was cloned and sequenced according to standard protocols known in the art. This sequence was designated at LP2-3$^+$.

[0147] GenBank blastx searches conducted with the above sequence translated in all 6 reading frames indicated that LP2-3$^+$ likely encodes a member of the major intrinsic protein family. This family of proteins encodes membrane channels for the transport of water and/or ions across cell membranes. They may play a significant role in osmoregulation and may play a role in the cellular responses to water and salt stresses. As is known in the art, the MIPs are induced by dessication, flooding, and high levels of the plant hormone ABA. In contrast, the LP2-3 sequence was not detected in desiccated late-stage embryos which have high levels of ABA and, thus, appears to be regulated by some embryo-specific signal.

EXAMPLE 3: Hypothesis Development for Improved Protocols

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[0148] Currently the improvement of tissue culture practices arises via hypothesis, evaluation and adoption. Hypotheses arise from observation of size, shape, weight, etc. and physiological measurement of ion or sugar content (Figure 6, box 1). These observations are limited in scope and this limits the improvements that can be made to the tissue culture process. Gene expression is closely linked to metabolic condition, thus the observation of which genes are induced or repressed under a given growth condition, naturally, on the tree, or in a culture vessel, provides insight into the metabolic state of the embryo. This information can be used to create new hypotheses that can be evaluated by modifying tissue culture.

[0149] To this end, mRNA levels of two cDNAs (LPZ-202 and LPZ-216), similar to "Late Embryogenesis Abundant" (LEA) proteins, identified in other plants, were monitored. These genes are induced by the plant hormone ABA. Two peaks of mRNA were observed in these clones rather than the typical single peak in most plants. (See Figure 4 for clone LPZ-216; clone LPZ-202 is similar but data is not shown.) It was subsequently confirmed that two peaks in ABA activity are observed during development and that these correspond in timing to the elevation in mRNA for LPZ-202 and LPZ-216. Thus mRNA abundance profiles are providing insight into embryo physiology. (See Figure 7) The effect of giving two pulses of ABA to our somatic embryos is assessed; a tissue culture modification that we might not have considered as important had the gene expression data been unavailable. Internal data shows fluctuations in the abundance of mRNA for cDNAs listed in this collection (data not shown.)

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Zygotic and Somatic Loblolly Pine Embryos

[0150] Loblolly pine cones were collected weekly from a breeding orchard near Lake Charles, Louisiana, and shipped on ice for experimentation. Embryos were excised and evaluated for developmental stage (Pullman et al. 1994). Stage 9 embryos were separated by the week they were collected - 9.1 (week 1), 9.2 (week 2), etc. Staged zygotic embryos were sorted into vials partially immersed in liquid nitrogen and stored at -70°C. Somatic embryos for loblolly pine were initiated as described by Becwar et al. (1995) or with minor modifications. Somatic embryos were grown, selected, and staged as described by Pullman et al. (1994) and stored at -70°C.

cDNA Probe Preparation and Hybridization

[0151] 30 ng of purified Lea protein cDNA fragments was labeled with ^{32}P dCTP using the Ready-To-Go cDNA Random Labeling kit (Pharmacia). The labeled cDNAs were purified using NICK Column (Pharmacia) and heat denatured for hybridization. The RNA slot blot was pre-hybridized in hybridization buffer (0.5 M sodium-phosphate, pH 7.2, 5% SDS, and 10 mM EDTA) at 65°C for 2 hours in a hybridization oven (Model 400, Robbins Scientific, Sunnyvale, CA) and the hybridized in the same conditions with the cDNA probes. After hybridization, the membranes were washed at 65°C in 0.2x SSC and 0.1 % SDS. Each wash was 15 min. The membranes were then exposed to Image Plate.

[0152] The probes can be stripped from the RNA slot blot by pouring boiling 0.5% SDS onto the membrane twice and incubating without heating for 30 min. The stripped blot was then exposed to Image Plate for overnight to check the completeness of the de-probing before next round of hybridization.

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[0153] To ensure the equal loading of the each RNA sample, the same membranes were stripped and hybridized with a ^{32}P-dCTP labeled 26S ribosomal rDNA fragment. These results were used as controls to normalize the Lea protein gene expression levels.

[0154] As a means of evaluating the usefulness of these arrays, we followed the expression of three cDNAs that have strong sequence similarity to late embryo-abundant proteins, (Lea) proteins from cotton (Baker et al 1988). Lea proteins and mRNAs appear in embryos at a stage when ABA is high and the genes can be induced in vegetative tissue by application of ABA. The transcript level of Lea genes LPZ-202 and LPZ-216 showed two peaks, rising from stage 5 and returning to a base line about stage 9.2 then rising again around stage 9.5. (See Figure 4 for clone LPZ-216).

[0155] To confirm the fluctuation in lea transcript levels by Northern analysis. RNA was extracted from zygotic embryos at different stages of development. A pine 'dehydrin' cDNA from the North Carolina State University cDNA collection (http://www.cbc.med.umn.edu/ResearchProjects/Pine/DOE.pine/index.html) was used as probe for some experiments. Dehydrins are a class of lea protein, originally identified as water deficit inducible proteins. Since the expression of this class of protein is well characterized, in contrast to our lea genes, the dehydrin expression profile could act as a reference point. After probing with dehydrin, blots were stripped and probed with a 26S rDNA probe from Arabidopsis to check the loading of the original gel. The normalized expression pattern of dehydrin in the zygotic embryogenesis is illustrated in the top panel of Figure 4. The expression of the dehydrin gene was induced at stage 5 and reached a peak at stage 6. It declined at stage 7 - 8, just prior to

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the onset of the desiccation. Then the mRNAs level remained low from stage 9.1 through 9.5. The dehydrin mRNA levels rose again late in development, from stage 9.6 on, apparently dropping in very late development. A similar pattern of expression was observed in a parallel experiment when our lea-like clone, LPZ-216, was used as a probe.

[0156] This pattern reveals two significant peaks at the early development of the embryos and high expression levels for the stage 9.6 and beyond. The expression pattern of these two lea genes in loblolly pine embryos is consistent with the changes in ABA concentration observed in pine during embryogenesis. (See Figure 5)

EXAMPLE 4: Evaluation of Metabolic State of Somatic Embryos as Compared to Zygotic Embryos for Fitness Determination

[0157] The model and goal for somatic embryogenesis is to produce an embryo that in vigor, germinatability, etc., resembles a zygotic embryo. Standard measurements reveal relatively little about the embryos; thus the metabolic state of somatic and zygotic embryos is unknown. The metabolic state of zygotic (natural) embryos can be evaluated by DNA arrays containing the cDNA clones described in this application. A database of mRNA levels for the genes represented on the DNA arrays can then be established. Embryos growing under a new tissue culture protocol (Fig.6, box #2) can be evaluated by DNA array southerns (Fig.6, box #3). The array elucidates patterns of gene activity and reveals whether those patterns are similar to the natural state (Fig.6, box #4). The germination, or further development can be checked (Fig.6, box #5) to confirm the conclusion. Where a link between specific gene activity and embryo performance has been demonstrated, protocols can be modified with efficiency as seen in Figure 6, box 6.

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[0158] To illustrate this process, elevation of plant hormone ABA in maturation medium was evaluated as a protocol modification, as described below. This modification proved beneficial, elevating the number and quality of the embryos produced. The mRNA abundance for cDNAs was assessed by DNA array using RNA isolated from control and elevated ABA conditions; several differences were observed in the mRNA levels of specific genes. Further, abundance of mRNA in the elevated ABA condition, more closely resembled the mRNA abundance observed for the these same genes in zygotic embryos. Thus a protocol which produces higher quality embryos produces, in these embryos, a mRNA profile that more closely resembles that observed in natural embryos.

Zygotic and Somatic Loblolly Pine Embryos

[0159] Loblolly pine cones were collected weekly from a breeding orchard near Lake Charles, Louisiana, and shipped on ice for experimentation. Embryos were excised and evaluated for developmental stage (Pullman et al. 1994). Stage 9 embryos were separated by the week they were collected - 9.1 (week 1), 9.2 (week 2), etc. Staged zygotic embryos were sorted into vials partially immersed in liquid nitrogen and stored at -70°C. Somatic embryos for loblolly pine were initiated as described by Becwar et al. (1995) or with minor modifications. Somatic embryos were grown, selected, and staged as described by Pullman et al. (1994) and stored at -70°C.

Mass Isolation of Genes Differentially Expressed in Loblolly Pine Zygotic Embryos

[0160] The following RNA differential display method is sensitive enough to produce banding patterns from one mid- to late-stage embryo or 10-20 early stage embryos. This technique, which extracts mRNA directly from tissue using oligo(dT)

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beads, avoids losses inherent in conventional RNA extraction methods, is fast, reliable, and inexpensive. Differences in gene expression during development, as well as between somatic and zygotic embryos, can be easily detected.

[0161] To achieve these results, 50-100 µl lysis buffer containing 100 mM Tris-HCl, pH 8.0, 500 mM LiCl, 10 mM EDTA, 1% SDS and 5 mM DTT was added to 10-100 mg of staged embryos in a 1.5 ml tube. The mixture was ground thoroughly with an electric drill containing a plastic pestle bit (VWR, Cat# KT95050-99) that had been sterilized by autoclaving. An additional 50-100 µl lysis buffer was added and ground briefly. The grinder and vortex was washed with 100 µl lysis buffer. If multiple samples were processed, each is stored on ice until ready for the next step. The grinding tip was washed with sterile water and dried for the next sample.

[0162] After all the samples were ground, they were spun at 4°C for 15 minutes in a bench top centrifuge at 14,000 rpm. 8 µl oligo(dT) coated Dynal beads (mRNA DIRECT Kit, Dynal, NY) was placed in a 1.5 ml tube. The Dynal beads were washed twice with a 100 µl of the above mentioned lysis buffer and suspended in an equal volume of the lysis buffer used in tissue grinding. If more than one sample is handled, the beads for all the samples can be washed together and dispensed in several 1.5-ml tubes. The cleared embryo lysate (after centrifugation) was added to the beads and mixed well.

[0163] The mixture was then incubated on ice for 5 min., placed on a magnetic stand (Promega) for 5 min., and partially dried by careful removal of the liquid. To this, 100 µl of washing buffer with LiDS containing 100 mM Tris-HCl, pH 8.0, 0.15 mM LiCl, 1.0 mM EDTA, and 0.1% SDS was added. (mRNA DIRECT kit.) The mix was

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transferred to a 200 µl PCR tube. The beads were washed once with 100 µl washing buffer with LiDS and once with 50 µl washing buffer containing 100 mM Tris-HCl, pH 8.0, 0.15 mM LiCl, and 1.0 mM EDTA. (mRNA DIRECT kit.) The beads were then washed quickly with 20 µl 1x RT Buffer (25 mM Tris-HCl, pH 8.3, 37.6 mM KCl, 2.5 mM MgCl2, and 5 mM DTT) and 20 µl RT Mix containing 1X RT Buffer and 20 µM dNTP was added. The tube was heated at 65°C for 5 min. and cooled to 37°C. 1 µl MMLV reverse transcriptase (Promega) was added and the mixture was incubated at 37°C for 1 h. with occasional shaking. Next, 20 µl of water was added to the RT reaction, mixed and a 1.0 µl to 20 µl aliquot of the PCR mix containing 1x Perkin-Elmer PCR buffer, 2.0 µM dNTP, 1.0 µM T12VN, 0.2 µM arbitrary 10-mer, 1 unit AmpliTaq (Perkin-Elmer), 50 µCi α^{35}S-dATP (Amersham) was taken. PCR using temperature settings of 94°C 30", 40°C 1', 72°C 2', 40 cycles, and 72°C 10' extension was performed with the Perkin Elmer 9600 Thermal Cycler. All PCR product was run on appropriate gels for band visualization.

cDNA cloning of Differential Display Bands

[0164] All dried gels were marked with radioactive ink prior to film exposure for proper alignment between the X-ray film and the dried gel plate. Appropriate bands were marked by puncturing. A scalpel blade was used to score the gel around each band to be excised. The excised gel pieces were placed into a PCR tube containing 2 µl water. PCR was performed using a 50 µl PCR mix (same as for differential display with the following modifications: the primer concentration was 1 µM, and the dNTP

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concentration was 200 μM; no α^{35}S-dATP is added.) The cycle settings were the same as above.

[0165] A portion of the PCR products was run on a gel to determine amount and size of PCR products; DNA that did not correspond to the size of the original differential display band was discarded. The remaining PCR fractions were purified using CHROMA SPIN-100 columns (Clontech, Palo Alto, CA) according to the manufacturer's instructions. The purified PCR fragments were cloned into the pCR2.1 TA cloning vector (Invitrogen) according to Invitrogen cloning protocols supplied with the vector. The only variation from the standard protocol was an increase in the molar concentration of PCR product to vector (over 100-fold); multiple insertions were not found to be a problem. All ligations were performed at 16°C overnight, transformed into E. coli strain DH5α, and plated onto LB with X-gal/IPTG.

[0166] Five colonies were chosen for PCR verification; PCR products of expected size were selected. About 10 μl of the 30μl PCR reaction was simultaneously digested with *Nla* III and *Mse* I overnight at 37°C (a 5 h digestion was used as well.) cDNA clones were selected according to the colony PCR and the restriction enzyme digestion pattern.

[0167] The differential display protocol for finely staged zygotic embryos of loblolly pine as described above, has produced more than 600 differential display patterns and more than 60,000 bands. Within that set of bands, we have identified bands that increased and/or decreased during embryo development. From those bands, cDNA clones of this invention were isolated and sequenced.

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Detection of Gene Expression by Micro-Array Assay

[0168] In order to verify expression patterns of the cloned DNA in loblolly pine embryos a micro-array assay was developed. The cloned cDNAs were amplified by PCR and adjusted to equal concentrations (0.1 μg/μl). The cDNAs were then dispensed in the wells of a 384-well plate, denatured in 0.3 M NaOH at 65 °C for 30 min. and neutralized with 2 volumes of 20x SSPE mixed with 0.00125% bromophenol blue and 0.0125% xylene cyanol FF (5% gel loading dye). The denatured DNAs were then blotted on to Hybond N+ membranes (Amersham) as arrays using a VP 386 pin blotter (V&P Scientific, Inc., San Diego, CA). Each DNA was dot-blotted four times as a quartet on the membrane. An example of quartet spotting is seen in Figure 7. Each dot is about 1.2 mm in diameter and contains about 3 ng of DNA. DNA was then cross-linked to the membrane at 120,000 mJ/cm2 in a CL-1000 UV-linker. (Strategene, Inc., Upland, CA.) The dot image of each membrane was scanned, numbered and saved in computer for later use in data digitizing.

[0169] The cDNA array membranes were pre-hybridized in hybridization buffer (0.5 M Na-phosphate, pH 7.2, 5% SDS, and 10 mM EDTA) at 65°C for 30' in a hybridization oven (Model 400, Robbins Scientific, Sunnyvale, CA) and then hybridized under the same conditions with total cDNA probes made from mRNA. The membranes were washed twice at room temperature in 2x SSPE and 0.1% SDS, twice in 0.5x SSPE and 0.1% SDS, and twice in 0.1x hybridization buffer. Each wash was roughly 20 min. Each membrane was then exposed to Kodak Biomax MR films.

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202-408-4000

[0170] The total cDNA probes referred to above were made by initially creating the first strand cDNA. This was accomplished by mixing loblolly pine embryos (0.05-0.1

gm fresh weight) with 100 µl lysis buffer (containing 100 mM Tris-HCl, pH 8.0, 500 mM LiCl, 10 mM EDTA, 1% SDS and 5 mM DTT) in a 1.5 ml Eppendorf tube. The mix was then ground with an electric drill as described above. Another 100 µl lysis buffer was added and the lysate was ground again briefly. The drill pestle was washed with 100 µl lysis buffer that was pooled with the lysate. After centrifugation at 14K at 4°C for 15 min. in a Beckman bench top centrifuge, the clear embryo lysate was mixed with 10 µl Dynal beads washed twice with lysis buffer. The suspension was incubated on ice for 5 min., with occasional mixing to allow binding of Poly (A) RNA to the oligo (dT) on the beads, and then left on a magnetic stand at room temperature for another 5 min. The liquid was removed and the beads were moved to a 0.2 ml PCR tube by suspending in 100 µl lysis buffer.

[0171] The beads were washed twice with 100 µl of washing buffer with LiDS and once with 50 µl of washing buffer. The mRNA was eluted from the beads in 6 µl water at 65°C for 2'. One µl T21VN primer (10 µM) and 1 µl SCSP oligo (cap switch primer, 5'-ctcttaattaagtacgcggg-3', 10 µM) were added to the mRNA eluate. The mixture was incubated at 70°C for 2' and cooled on ice. Three µl 5x First Strand Buffer, 1.5 µl DTT (20 mM), 1.5 µl dNTP (10 mM each) and 1 µl MMLV Superscript II (Gibco BRL) were added to the mRNA-primer mixture followed by incubation at 42°C for 1 h to synthesis first strand cDNAs. The cDNA was heated to 72°C for 1 min. to degrade RNA and then diluted to 100 µl with water. The lysis buffer, washing buffer and Dynal beads are components of the mRNA DIRECT kit (Dynal, NY). The first strand buffer (5x), 20

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mM DTT and 10 mM dNTP are components of the SMART PCR cDNA synthesis kit (Clontech, Palo Alto, CA).

[0172] The first strand cDNAs synthesized as described above contains a T21VN sequence at their 5' ends and the SCSP sequence (see "SMARTTM cDNA, Clontech, Palo Alto, CA) at their 3' terminals. Total cDNA probes were made by PCR amplifying the first strand cDNAs using SMART cDNA PCR (Clontech, Palo Alto, CA) in the presence of labeling agent. Five 5 μl first strand cDNA solution was mixed with 5 μl 10x KlenTaq PCR buffer (Clonetech), 5 μl dATP + dGTP + dTTP (5 μM each), 1 μl T21VN primer, 1 μl SCSP oligo, 1 μl KlenTaq Mix, 5 μl 32P-dCTP (10 mCi/ml, Amersham) and 27 μl water. The PCR was performed using the setting of 94°C 2', 15 cycles of 95°C 15", 52°C 30", 68°C 6'. The PCR products were purified using NICK column (Pharmacia) according to the manufacture's instructions.

[0173] Currently, high-density array Southerns for both somatic and zygotic embryos at all the developmental stages have been performed. The dot array Southern data indicate that gene expression of late stage somatic embryos resembles middle stage zygotic embryos; many transcripts present during late zygotic embryogenesis (ZE) are absent in somatic embryos and late stage somatic embryo gene expression patterns resemble the patterns of middle stage zygotic embryos.

[0174] Cairney et al. (*In Vitro Cell. & Devel. Biol.- Plant.* 36:155-162 (2000); *Appl. Biochem. Biotech.* 77-79:5-17 (1999)) have discussed how this gene expression information may be used to improve the process of somatic embryogenesis; the references are incorporated in their entirety. As shown in Figure 2, the high-density array Southerns allows rapid evaluation of embryos subjected to protocol changes.

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Following the expression of a known gene permits inferences about metabolism and is very valuable in developing media-improvement hypotheses. Further, detailed gene expression studies may help by providing an understanding of the timing and location of gene expression (e.g., *in situ* hybridization). The isolation of key genes also provides the ability to monitor the expression of these genes as stage specific markers and allows protocol variations to be quickly evaluated.

EXAMPLE 5: Identification of Markers for Superior Performance in Tissue Culture"

[0175] The evaluation of tissue culture modifications for pine somatic embryogenesis, depicted in Figure 8, is typically a lengthy process. However, where molecular tools are available, potentially improved media or genotypes can be discerned more rapidly, thereby avoiding the months of costly evaluation. (See Figure 8) Table 5 illustrates this proposition.

[0176] Table 4 describes several publicly available clones, *Lec*, *Fie*, and *Pkl*, used to provide a representative model for this example. Any clone within Table 1, SEQ ID NOS: 1-327, can be substituted for those in Table 4 to assay increased performance in tissue culture. Any promoter within Table 1, SEQ ID NOS: 328-334, can be incorporated with those in Table 4 or SEQ ID NOS: 1-327 to assay increased performance in tissue culture. In this scenario, Table 5, a representation of the information contained in Figure 9, shows performance of selected genotypes (260, 480, 499, and 500) in various media (1133 or 16) determined by the total number of embryos produced per medium as described by Pullman and Webb (1994), incorporated herein. Embryo maturation was determined by the presence of recognized morphology according to methods previously mentioned above. (Pullman and Webb, (1994))

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Genotypes that produced high, medium, and low numbers of embryos were selected for RNA extraction. Gene expression assays, such as DNA arrays, Northern blots, slot blots, etc., were used in attempt to correlate embryo performance with mRNA abundance for selected genes. In the example shown in Figure 9 and Table 5, expression of loblolly pine genes, designated as *Lec*, *Fie*, and *Pkl*, obtained from the Pine Gene Discovery Project, was evaluated. The preliminary correlation appears to be that the high levels of the *Lec* gene's mRNA correlates with greater number of pine embryos. (See table 5.) These experiments can be further expanded to incorporate additional or alternative genotypes with the prospect of identifying a large collection of gene indicators of good or poor performance in tissue culture based on high or low mRNA levels. It is clear from the above that this approach, using the sequences disclosed in this application, can evaluate a genotype entering tissue culture, saving both time and expense.

Somatic Embryos

[0177] Immature zygotic seeds were collected from loblolly pine genotype 260 (mother tree BC-3, Boise Cascade). Somatic embryos were initiated as described by Becwar et al. (1990) or with modifications in media mineral composition. The early stage somatic embryos were grown in cell suspension culture medium 16 and sub-cultured every week (Pullman and Webb, 1994). The embryos collected from the suspension, which include stage 1 and stage 2 somatic embryos, are referred to as stage S embryos. At the end of the subculture week, the somatic embryos in the suspension were settled in a cylinder and transferred to maturation medium 240

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(Pullman and Webb, 1994). Resulting somatic embryos were selected, staged, sorted into vials containing the same stage, and stored at -70°C until analyses were performed.

Probes

[0178] For the following example analysis RNA was isolated from embryos at different stages in development, early stage somatic embryos and late-stage somatic embryos. The cDNA probes used in this example are not contained in the SEQ ID NOS: 1-327, but rather, are generic, publicly available pine sequences obtained from the Pine Gene Discovery project located at (http://www.cbc.med.umn.edu/ResearchProjects/Pine/DOE.pine/index.html). These clones are homologs to the well-studied *Arabidopsis* genes that have been shown to have significant influence on embryo development in this plant. The pine clone names (first column) and corresponding references for the *Arabidopsis* homologs are shown in Table 4. The three clones listed, *Lec*, *Lie*, and *Pkl*, are for representative purposes within this example and it will be clear to one skilled in the art that any of the SEQ ID NOS: 1-327 could be substituted for those here as all will help identify conditions for improved performance in culture.

[0179] Probes were made by preparation of DNA using Wizard Minipreps (Promega, Madison, WI) and cDNA inserts isolated by restriction enzyme digestion. For the cDNA probes, 50 ng of the isolated cDNA insert DNA was used to make ^{32}P-labeled probes with Ready-To-Go DNA labeling beads (Amersham Pharmacia Biotech) according to manufacturer's instructions. Blots were prehybridized (7% SDS, 1% BSA, 0.25 M $NaPO_4$ (pH 7.2), 1.0 mM EDTA) for 3 hours at 65°C and hybridized in fresh buffer at 65°C for 12 to 18 hours (4). Each blot was washed 6 times with the following

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conditions: 1) RT, 2X SSC, 0.1% SDS, 15 min; 2) RT, 2X SSC, 0.1% SDS, 30 min; 3) 42°C, 0.2X SSC, 0.1% SDS, 15 min; 4) 42°C, 0.2X SSC, 0.1% SDS, 30 min; 5) 60°C, 0.2X SSC, 0.1% SDS, 30 min; 6) 60°C, 0.2X SSC, 0.1% SDS, 30 min. Blots were exposed to a phosphorimaging plate for 10 minutes. Screens were read with a BAS1800 (software v1.0) and images were manipulated with ImageGauge (v2.54) (Fuji Photo Film Co., Ltd., Kanagawa, Japan).

[0180] The hypothesis tested within this example is that genotypes that produce large numbers of embryos have high *Lec* expression and low *Pkl* expression, poor genotypes have the opposite pattern, and that *Lec* and *Pkl* expression act as indicators of embryogenic potential. Figure 9 shows that *Lec* is not expressed in late stages of embryogenesis in somatic embryos. The *Lec* gene is expressed throughout embryogenesis in *Arabidopsis*. The blot reveals that the *Lec* gene is a useful early expression marker for embryogenesis. One interpretation of these results is that the somatic embryos do not express *Lec* in the manner that *Lec* is expressed in zygotic embryos, i.e. the use of *Lec* expression has highlighted a defect in gene expression in somatic embryos. This defect could be used to identify desirable genotypes, i.e. those likely to progress through development and produce a large number of healthy plantlets compared to undesirable genotypes that will cease development prematurely or produce low numbers of plantlets. This is an example of the principle described pictorially in Figure 8.

[0181] The results described in the previous section of Example 5 reveal ways in which gene expression analyses can be used to improve somatic embryogenesis based on several genes. However, this principle applies as well when the assay is

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expanded to determine the expression of hundreds or thousands of genes simultaneously (e.g. by DNA arrays). We can create hypotheses which state that expression of a single specific gene can be used to determine the potential of a culture, or hypotheses that state that the expression of a group of genes (e.g., hypothetical genes A, B, C, D, E, F) acts as an indicator of high embryogenic potential. For example, all these genes may be expressed at a high level in cell lines that produce large numbers of embryos, thus we would select cell lines which exhibited this characteristic. Alternatively specific levels of expression for genes A, B, C, D, E and F may be required and a combination of high and low expression of particular genes will identify desirable cultures. Alternatively, experience will determine that certain exceptions can be tolerated.

[0182] While the previous paragraphs discuss numbers of embryos produced, the principle applies to ANY desired characteristic: by establishing a correlation of gene expression with e.g., germination potential, embryo size, growth of plantlets in their first year, disease resistance of mature plants, environmental hardiness or wood quality. Any trait where could be evaluated by these gene expression assays and correlations with gene expression established, resulting in a molecular tool which could be used to predict desirable characteristics. Explicitly, we could use these gene expression tools to select cell lines which will produce high quality plantlets months before they grow into plantlets, or cell lines or juvenile plantlets which will produce hardy trees with desirable wood quality, years before these traits are expressed.

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:1	Late	LPS-001	GGTACTCCACCGTAATAACCCTTGGGAAATAGCCTATGATCCAGGGGAGGCAACC ACCTATATCATTGACAACAGCGAAAAATGTGGCGCAAGAAGTTTCACATACAATTCA TGGTTACAAAGATCACATACCAGGTGTTGGAGCAGATTCGATAGATATTGAAGATAT GAAGCCAAGGAGTGGAGCAGTTATTGAAAAGGGCACAAAAAAATTTGCCATTTACA AAGATGAAAATGGGCTGATTCACAAATACTCGGCAATATGCCCACACATGAACTGT ATTGTGAAATGGAATCCTATAGACTCAACTTTCGATTGCCCCTGCCATGGTTCAATG TTTGATAATCTGGGTCGATGCATCAATGGACCTGCCAAGGCGGACCTATTTCCCGA AGATTAACGATAGTTGTTTGTACATGTAATTATCTTGATATTGTATATATATGTATTTA AATTATACAGTACAATAAATCCATGTTTGCAGGCTATTTCTGCTTGATAATTTAGCTC CAGATTTATACATAACCAGTTTATTTGGCTGTTTTTCCCCTGGCAAAAAAAAAAAA
SEQ ID NO:2	Late	LPS-003	003GGTACTCCACAGAAAGAAATGATTTGACAGAAAAAGAGAGCTGTAGGATTGGGT AAACCCTGCAGTGGATATATACAATGTATATGTACTCTGTCTGTTTTTCTGTTATTTG ACGGAAATAAAAACGCCATAGCGACGGATGACTGTAAATCCTTAGGGACGGATGAC TGTAAATCCTTAGGTTGGAAGATTACAAACGACATATGGGTCTTTCAATTTTCAGAT TTCTGTAAGACTTACATTTCAAAGACTGTTTGGATGGGCAAAAAAAAAAAA
SEQ ID NO:3	Middle	LPS-004	GGTACTCCACCAGAATGCCGCAGTTTAGTTCTCTAAAGCAAGCAGTAAATTAATTTT GTCAAAATCTAAAGAGTGTATAGTATCAGTGGGTTTGTATTTCCTAGTTTGCCTACA ATAACGATGGGGATTCACCAGTTTTTGTAGAATTTGCAATCATCGGATGACAATTTC AAAGTTTTCTCTAAGTCACCCGCATTGATATCGAGAAGCCTTCCATTTTCAATTATTT AATATCAGAAAATCTTTTCAGTTGGCAAAAAAAAAAAA
SEQ ID NO:4	Middle	LPS-006	AGCCCAGCTGCGAAGGGGATGTGCTGCAAGCGATAAGTGGTAACGCCAGGTTTCC AGTCAGACGTGTAAACGACGCCAGTGATGTATACGAATCACTATAGGCGATGGCCT TCTAGATGCATGCTCGAGCGCCGCAGTGTGATGAATTGCAGAATCGGCTGGTACT CACGGGCTAGAGAAAGGCACAAGCACTTTTTGTCATTTTAGGATCAGAGGCATTCA GGTATAGGAAGGGTGGCTCAGATAGGCAGATGGATCGGCATTTTGCCCAGTCATG AAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCTTTGTGCCTTCT GGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATATGGTTTGTCACT GAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAAGTGATTATTTG TTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTACCAGTCAACA AACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAACGTGTAG CTAATTGTTCTGGCAAAAAAAAAAAA
SEQ ID NO:5	Middle	LPS-007	TCCAAAATACAAAGGCTTTATTTGCATCATGATATAATACAAAGTAAGAAATTTACCC AACTGTTTAACCTAATAATAATACAAAGGAAGCATTTTACCCAACTCTTTAACGTAAT AATACCAAAGAGTGGAATGCTTTATTGACCAGCAAGACCTTGAAATTTTTATAACCA ATGCCCATCAACAGAGCCTTTCTTAAAAAACGCAAAGCCCAGCTCTGTCACCTTATT AGTTAGTATAAACTGACATTCTTCCAAGCTTGTGTGCGCAGAAACAATAAAGAACTT CACCTTGGTTTAAAGAACGTGCCATGAAGAAAACGTCCCAAGAAAAATGAAATGGC TCCTTCGACCATTCAGTCCTCCCTAGAAAAATCAAAAGACTCCTTCGACCATTAGGT CCTCCAATTGGGCATCTAACTACAAGCGGTC
SEQ ID NO:6	Middle	LPS-008	GGTACTCCACGGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGGATCA GAGGCATTCAGGTATAGGAAGGGGTGGCTCAGATAGGCAGATGGATCGGCATTTT GCCCAGTCATGAAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCT TTGTGCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATAT GGTTTGTCACTGAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAA GTGATTATTTGTTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTA CCAGTCAACAAACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGT AAACGTGTAGCTAATTGTTCTGGCAAAAAAAAAAAA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:7	Middle	LPS-010	ACGACGTGTAAACGACGGCCAGTGATTGTATACGACTCACTATAGGGCGATTGGC CTTCTAGATGCATGCTCGAGCGGCCGCAGGTGATGGATATCTGCAGAATTCGCTT GGTACTCCACGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGATCAGA GGCATTCAGGTATAGGAAGGGTGGTCAGATAGGCAGATGGATCGGCATTTTGCCC AGTCATGAAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCTTTGT GCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATATGGTT TGTCACTGAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAAGTGA TTATTTGTTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTACCAG TCAACAAACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAAC GTGTAGCTAATTGTTCTGGCAAAAAAAAAAAA
SEQ ID NO:8	Middle	LPS-011	GGTACTCCACGAAGCAAAAAGAGTCAGGGGAATGAAGATGGGGGGCTCCGACAAG AAGCGGATCAGAGAAGAGCAGGAAATGAGTCCACCTGAGGAATCCTGGAGACAGA AACAGGGGCGTTTAATGGAGTTTGAGGCAGGGATGGCCTATGATAAACCTGAAAAT GCCGGTGCAGGTAATGAGAATTTGCCAGAGTTTTGCTCTCTTTCAAATGAGTACTC GATGTTATTGAAAGATCCATGGAGTTGGGAGGATAGCACTGGTTTCGGAATCCGAA GCTTAGCTGCTGTCAGGAAGCAGTCTTGTATATTGGACTATCTCCATGATTCTGCT GTAGATAATCGCTGTGAAAAGGATTTTGCCGAGCAGCACAAGGTACAGGAAGAGG AGGATTGTTTGAGAAGGTCTCTTTTTGAAGCCACAGATGATCAGCTCTGGAGGCTT CAGAGTCTTTGCAGGATACAGAAGGTCTGTTTCCTCTGGATTCCGTGGGTAGCCAT GATTGCACGACCTTGTTGCAGGATGAGAGCATTGTTCAGGGCGCTGCTTCTTACTT CAGAATTTGGGAACAGGATGATGGTCACAAGGATGCCAAAATTCATGAAGATGGCA TTGGTTTTGTGTATGGGAGTGGGATCTCGGATTGGATTCGGAGGGCTCCCTCGAA TCAATCTGAGTTTTCTGAATCTGTTGAATTTGAAAGCTCTATGTTTTCACTGTAATTT GGGTCTTTTTAATTTCTTCCTATGTAATTTGGGTGTTTCTAATTTCTTCCTTCAGCAA AAAAAAAAAA
SEQ ID NO:9	Middle	LPS-012	GGTACTCCACCATATCCAGGTAAACAAGGGAAAACAGAGTCAGCTTCTAGTATGTT GTATGCCTTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTGA TCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCATTA GCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGATAACTTCTAGAGCATTTT TCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTTTACTTTCTTAAACTGTA CTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAA
SEQ ID NO:10	Middle	LPS-013	GGTACTCACCATATCCGGTAACAAGGGAACAAGTCAGTTTTAGAAAGTGGACCCCC GGTTCCGTCGTTTTCTTGATCTCGGAGCCAAGCAAGTGGATGTGATCACTAAATGT TGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGGTCATTAGCACAGAAGCTA TTGGAGAAATGATTATGGTATTCCACCATATCCAGGTAAACAAGGGAAAACAGAGC TCAGCTTCTAGTATGTTGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCC AAGCAAGTTGAATGTGATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTG TCTCTTTGGTGTCATTAGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGAT AACTTCTAGAGCATTTTTCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTT TACTTTCTTAAACTGTACTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAA AAAAAAA
SEQ ID NO:11	Middle	LPS-014	GGTACTCCACCATATCCATGTAAACAAGGGAAAACAGAGCTCAGCTTCTAGTATGT AGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTG ATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCATT AGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTACATAACTTATAGAGCATTTT TCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTTTACTTTCTTAAACTGTA CTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAA
SEQ ID NO:12	Late	LPS-015	GGTACTCCACTAGACCGGGTAGGGTCTCTCCATGGTTTTGCGACTTAGGTTAGGTG TCCTGTTCTGTTAATGATTTTGAGGTTTTGTAATTGTGAGTATGTTTCCAGGGTTTT GAACCTGGGTACTCGGCCTTTGTTGGAATGTAGTCTGGTTAATTTATATGTATATGT AACCTTGGGGTTTCGAGCCCAGTTCTCTGTTCTTCTTGAAATGAAATGCGATTTGTT CTAAAAAAAAAAAA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:13	Late	LPS-019	ATATATACGTATGGTATTCCACAGCATGAACTCTTCGACATTATATGCTTGTTATAGT TTTTAAGAGAGGAGACTTACCTCACACATGTACAGCTTTTTATTGTCGTGCTTTCAG TTGATGGATGATTGTTGTAGTCCTGTCATTGGTTGGACAATTTTCATCATCCTAAAG ATCCAAGAATTCATGTGGCAAGAAACTTTAATAAAGTCAAATATAATCCGATGACGT AACCCTAAAAAAAAAAAA
SEQ ID NO:14	Late	LPS-020	GGTACTCCACTAGTGATCGATTCTCTGTATGTGACGCTGCGCGGCGGCTTATAGC GCTTCACTGAGAATGTACGGTATATTATGATTGATGTGATGGATTTGCTCCGCAGC TTCGGCTGTTGTATCTGCTCACTTCGGCGTATATATGTAATATGTTGCTTCTTCAGA GAGATGAACTTCCCCCTAAAAAAAAAAAA
SEQ ID NO:15	Middle	LPS-023	ATAGATCATTTTAAAGTTTCAGTGATTTGAATCTAATTCCACTGCATTTCCTCGCAAA CTGGCAGTCAAATAGTATTCCCTCTTTCAGTGACAGGCTGGCAGGTGTTTCATTCT TATACAAACATGATTATCATAATTCCATTAATTCATGGCGTTTTCTTTGCCAAAAAAA AAAAA
SEQ ID NO:16	Late	LPS-024	TTTTTTTTTTTTAGGGAGAAAGGTAACTTCAGCCAGCTTTCAAAGGCAACACCTACA AAAGGGGTGACTGAGAACTCAGACACAGACGACAAGTGATCATTCGGGCCAGATT TTTGTTGAGAGAGTTGTAGTGTGTAATTGATTCATTTCATACATTTGATATGCAAGC CTGTACAATAGCCTGTGACTGTTAAGGGCATTCTTTTGTCTCCCTGTTGCTATTTGG GTTTCCGGTGTGTTCATTTTCACTTATTTTTGTGTTTTAGCTGGAAGAATTTGAGAG GGTAGAATTGTGTCATCGCTATGGCTTGTGCATGACTCATGAGCCAGCAGTTGAAA CTTTTATTTATTAAGTTATAATACTATGTCTTGTCAATTCTCAATAAAAGATATTTTAT GCTGTTGGGCAGCATCTAAAATGTTTTGTATGTTAGCATAAAATCCCATTTTCTATA AGTTTTTGCCAAAAAAAAAA
SEQ ID NO:17	All	LPS-025	AGCAGGTTCAGTCAGACGTGTAAACGACGCCATGATGTATACGAACTCATATAGGG CGATTGGCCTTTAGATGCATGTTGACGGCCCGCAGTGTGATATTCGCAGATCGCTT TTTTTTTTTTTTAGGCATGGTGCGCGATGAGCTGATAGCGATGATGAAGACCAAGA CCACCAAAGGAAGATTCTTCAGAGCAAAAGCTACGGAGACAGAACCAGAGGACTC AAAGCCGGAATCCATTGGTGAGGTACCTGCAAATGTGTGATGGACTAACTAAGAAG GCTCCTTGAGAGGACCCATTAAGCACAGTGTTTTTAAGTCCCAAATTCTGTTGCAAT TCCGTTGAAAATCATTTTTACGATTTTAGGTATGATGTGTGCAATTTTAAAGTTGGAA TTATTGTGGGCAAAGGCTATAAGTGATTGTCTAATCCATTTAATTTATTATCTTTTGA CTAAGAGCATATCTAGGCTGGAAGAAATTAGGGCACATTAATGTAAGTTTTGAATTT GAACATTCTGGGTTTTGCAATGCAAAACACCACAAATATTTTATAATGTTAGAGGTG TACTTTTTCTGGCCAAAAAAAAAAAA
SEQ ID NO:18	Middle	LPS-026	GGTACTCCACCAATAATACTTGTCTGTTCTTGCTTCCCTGCTGATCCACTAAGCAGA TTATTTCTGTCCACCCCACTTTAGAGTCTCAGTTTGTAAAGCACTCCCTAGGAGCTA AACTCATTTCCAATGGATTAAAGCACTCCATAGGAGCTAAACTCATTTCCAAGGGAT TTTTGTCCATTTCTCTGTGCTAAAAAAAAAAAA
SEQ ID NO:19	Early	LPS-027	ATGTATACATATATGTGGTACTCCACACACTCAAATAACAGCATCACAATCAAAACA AGAAGGCGGCCAGAAAGCTTTAAAATGCTAAGCCTACAGGTAATATTCACAACTGC ATTAAGCACCCCGCTTCCTAGTTCTGAAGAAGCCAGAAAGCTTTAAAATGCTAAGC CTACAGGTAATATTCACAACTGCATTAAGCACCCCGCTTCCTAGTAGGCTAGTACTA GGACTAGGACCGCATTACCAGTTCCCTTATCTTCTACTCATCCTCTACAGGAAAAAC TATGACTAAAACTGCATTACCAGTTCCCTTATCTTCTCAACTCGTCCTCTACAAAAAA AAAAAA

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SEQ ID NO:20	Early	LPS-028	GGTAATTTCCACCCACCACGGGCTTTTTCAATTAACCCATTTCTACCACTCCACATT AGGGTTCTAAGTTTTGTGACTCACCCCCAATTTCGCTGATATTTTGCATTGCAGCTT GTTTATCTACAGGAAATGGCTAATCAGTACTTTCAGAATTTGGTTGCTTCTGTACAG GAAATGGATAATCAATCAGTACTTCTATACTTAAGTTGCTTACGCGGGGATCAGAG CCTTACTTCAGAAAATTGAATACATTTTCTTCTTTGTGTATGTATCAGGCATGGAATT ATATGTAGCATGCCATGGAATGCGTATTTACTAGATTATCTTTTAATTTAATACATAT GTTGCTTACTAATTTGTCCACAAAAAAAAAAAA
SEQ ID NO:21	Early	LPS-029	GGTACTCCACACACTCAAACAACAGCATCACAATCAAAACAAGAAGGCGGCCAGAA AGCTTTAAAATGCTAAGCCTACAGGTAATATTCACAACTGCATTAAGCACCCCGCTT CCTAGTTCTGAAGAAGGCCAGAAAGCTTTAAAATGCTAAGCCTACAGGTAATATTCA CAACTGCATTAAGCACCCCGCTTCCTAGTAGGCTAGTACTAGGACTAGGACCGCAT TACCAGTTCCCTTATCTTCTACTCATCCTCTACAGGAAAAACTAGGACTAAAACTGC ATTACCAGTTCCCTTATCTTCTCAACTCGTCCTCTACAAAAAAAAAAAA
SEQ ID NO:22	Middle	LPS-030	GGTACTCCACTATTAGATTGATGCAAGACCAACTGATCATGGCTAGGGTGTATTCA AGCATTTCCCAGGCTAGGAATAATCTTGATTTATACCATGAATTGATGCTTCGTATT AAAGAATGTCAACGTACATTGGGTGAGACTAATGCCGATTCTGATCTACCTCAAAG GTAATAATTTTTGCATTAGCTGCTTCTAAATCAAGAGTAGTAAGTGCTTCCATTTGC AAAAAAAAAAAA
SEQ ID NO:23	Middle	LPS-031	GGTACTCCACAAGGCATATATGGGCAATTGATTTTGCCTAGCCCAAATTCCTATTCA AGCTTGCGTATTTCTAAAAGATGCACTATTTTTTGTCCGAGTGTAGGTTTTGAATTC ATTGTAACATTCAGCAATATTAATTCAGGGGTAGCATTTCTGGCAAAAAAAAAAAA
SEQ ID NO:24	Middle	LPS-032	TTTTTTTTTTTTAGGGTAGAAAACCATGCTTCACTAACAAGGTATAAAATTACAATAT AATTCTGGGTGTAAACGACCTGATAGATGATCTGCAAGTGCCAGGAGGCAATATCT AGCAGAATACGTACAAATTAAATTGCCAAAAAAAAAAA
SEQ ID NO:25	Late	LPS-036	GGTACTCCACCAATGATCACCCATGTCCATTTGGTTAATTCAATGTCAAGATTTAGT AGTTCCGTATTCCCTTGGGTAAGCTGTAATGGTCCATTTGGGAACAGTCCATGTTT GGGACACAAGTTCAATAGAGATGTCATCCATAAATATGGGTATGAATCTCTTCCTTC CCTCTCCGCCCAATAATAAAAAAAAAA
SEQ ID NO:26	Late	LPS-037	TTTTTTTTTTTTAGTAGCAATAGCAATCCATTTTAGGGATCTGCAGATCAGTGACTAA GTGACCCCTACCCCCAAAGGATTAATTGTACTTTGGCTTAACCACAAAACCTGATTC AAAAAATGTGAAGTTTTTACCCATTAAATTAATTCCCAAAAGTAACTACAAATTCCAG AGTACATTTTTACCCAAAAAAAAAAA
SEQ ID NO:27	Middle	LPS-038	GGTACTCCACTATACAATATCAAGGCATATCTGCCGGTTGTTGAATCATTCGGATTC TCAAGCACTCTCCGTGCCGCAACTTCTGGCCAGGCTTTCCCTCAATGTGTGTTTGA CCACTGGGATATGATGGGATCTGATCCATTGGAACCTGGTTCCCAAGCTGGGCAG CTTGTGACTGATATCCGTAAGAGGAAGGGTCTTAAGGAGAGTATGACTCCCTTGTC AGAGTTCGAAGACAAGCTGTAGAGCTTTGCTATGTTTGCATGTCGGATGCTGTCAA GATTGAGGAACCTCCGAGTATTAAAACACAGTTTTGTGTGCTAGGACTATTTAAATT TATGCTATTCACGTATTTTTGTGATCTGTTATTTATGTTATTCACGTATTTTTGATTG GAAAATACTTTTTACAAGTCATCCATTAATCTTTTAAATGTTACATAATTCTCTCTTGT C
SEQ ID NO:28	Late	LPS-040	AAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTC GGCTTGGTACTCCACTATACAACATCAAGGCATATCTG
SEQ ID NO:29	M,L	LPS-041	CTTTTCTTCGTGCTTTTCGTGGAGTACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:30	Middle	LPS-042	GGTACTCCACAAAGTGAGATGAGTGATATGAGGTCAAACACGTAAATGACAATAGC TATTATTTCCCCACTTGTTTGTGGCTGTGTATATTATACTTCATTGTCAGGACTTTTG TATGGTTGAAGTTGCAAGGTTTTGGCAAAAAAAAAAAAAAA
SEQ ID NO:31	Middle	LPS-043	GGTACTCCACCTCCAGCTGCTTATCCAAGTACTACGGATAGTTCATACTCCTATTAT GCTTCTGCCAAGTGAACCAGAAGGCTTCTGTTTCTACACTAGCAAACTGATAGCTC GAGCATTCTCATTTACTAAGGATGATAATTCAAAATTGTAACATTGCAAACATCAGC AAACATCAGCATCAACTCTGTTACTATTACAAGCAATGGATGCGTCGCTGATGCTG CGGGAGAGTAAATTTTTAGTTTACTGCGGTTGGTAATTGAGTAGGTTGACTTACATT TCTGTTGTAAAGCCGTTGTCGGGCATTGTTTATCTGGCCGAGTTAGCGCCAGGAAG CTAAATGTACCAAATATTTATTTTTATTTTATTAAGAATATAAAATTTAGTCGTCTTCT GCTGCCCAAAAAAAAAAAAAAAA
SEQ ID NO:32	Late	LPS-044	ATGGCCATGGACTTATGACTTTCAAAACCCTAAAACCTATCTACAACTTTCCACGCT GAGATTTTCCGAGGAAGGCATTCTAAGCCATTCCCACCGTACTTTAATAAAATAAAA ACAAGAAGATAGTAAAGCTAAGCTACAACCTTCCGCCAAAAAAAAAAAA
SEQ ID NO:33	Late	LPS-045	GACCGCTTGTAGGAACACTAGCAGATTCCGGAACATAGGTACTTTGAACATCTTTC ACTCCTCACCATATGAATAGTGAGTCGATGGCGGCCTTAACAGTCGAGCATGCTTT GATTTCGTCTCTCTCTCTAGTGACCGAAATCAATCTCATTATATATGTCATTATGCAT TCATTCCCACTTCCTAACTTTCATTATTGTTCAAAACTTCGCCTTCCTGAAAATGCTA TAATAGTAGGGGAATATTGAAAAACTTCCGCCAAGCTAAAAAGGCACTTAAAGCAC CTGGATTTGAACCAGGATTTCCCACCCCGATGAGGGGGGGTGTCTTTCCATTGAG ACGATGCCTTACTCGGCAGACCCTGTGGGGGTCTTTATAGGTGACTTAATACTTAA GTATAGGACTTAAGAGAGAGGAAGCGACCGCCTCTCTGATCAAGCCTTTACGTGC GACGTGCCCAGGTAAAGGCTGATCTCACCAAATAATTCAGAGAAAGAAGATGACTC CACAGTAGCGAAACTCCTACATTGTCTTACATATCGTAACAAGCGGTC
SEQ ID NO:34	Middle	LPS-046	GACCGCTTGTGCCTGGTGTCCAAACTAGGACGCCTTAGTTTTCCTAAGAAGGAAAC CCAGGCGTTGACTTGAGGCAGACTTGTGCTTCTGGGTACTCTCATTCACTGCGTGA CCTTGAGAAAGGGACTTTACCTCCAGGATCCTCAAACTTCTTCTCTGTAAAATGAGC ATTGTAATAATTATATCCCAGGCTTATGTTGGGAATATTCAATAAATGCTCCCTTCAT TCTTTAAAAAATAAGTAAAGACAGCCTGAATGGGAGCCACGTTCTCATTCTTCTTTC TCTATGCAAAATGTATTGTGTAATGTTTGTGTACTAGTAGTTCAAGAGCAAATAAGT AGTTGGTTAATGGCTAACATATTTCTTAAATTTGTAACTGTTAAGATAAACATTGAAC AAGGAAAAAGATTCGTAACTGAAATGTAAAGTCATTTGACCCTGGATAGTCAATGAC AATCTTATTCACAGTGTAATAAGTAATTCATAACGAGATGATTATTATGAAATTATCA ATAGCCTGCTATATCACTTTATGTTTATGATCCACAAGCGGTC
SEQ ID NO:35	All	LPS-047	GACCGCTTGTGGAAGAAAAGAAAGAATCTCTTTCGGATTCAATAGGCGGTATGGGA GAGTCTGCTACTGCCTCTTGGATTCCAGGAATCCTAGAGCTGGGAGTATGAGTTGG AGATGATGAAGGTGTCTCTTACCTATTTCTTGAAGTGGATGGAGTTGTGAAAATCGA ACTTCTAGCTTCAGCTAAAAACCTTCCCCTAGAATCTCTTGCTCTATGCATATCATTT TTATTTTTTCTTTCAAGATAGGGTAATAATTCTCTTTCTGATCTTCCAGGTCACTCTA GGTGCAAGAAGAGAGCATAGTCAAGGAACTATTAAACCAATAACTTTCTCTTTTCTG ATCCTCCAGTTCACTCTAGGTACAAGCGGTC
SEQ ID NO:36	All	LPS-050	GACCGCTTGTGCAAAGTAGATACCGTCCTGTTCCGGTGAATTGAAGTACATTTTCA AAATGCGCTACTATGACATTTTATAGGATGTCTGAGTGTAAAATAATGGTACTGGTT GTTGCAAAGAATCTGATGTTTGGATGTATGGAACTATAAATAGATGTTATTTTCTGA TCCAGAAGGCTTTCCTTACCAACTGATTTCATCTTCAGAAACTAAAAGCTCTTGAAC TTGTGTAGATGGGGCTTGGTCATTGTAGTTTAAATGCATTATGTAGTGGCAAAAAAA AAAAGTTATAGCCTACGTTTCAAATGGATTTGCTCGACAATCAAATGAATTACAATT GAATATTCATGTATACCCAAATTTTAAATGTAGAATGACATCATCAATGTAGACAAAC ACCACTGTGCTTGTCCTTGATATCCTCTTTCACCATATAATTGGTGGCTTACTCAAA GTCACTATCTGATGCAACTACAAGCGGTC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:37	Late	LPS-051	GACCGCTTGTTCAATGCAGAATCTCGAAGAGATGTCTTGGACAAATACTGAACTGG CACGATTGGTGTAGTGCGGTTCAAAAGGCGCTCCAGATTCGTCTGGAACGAATCTT CATACGCTGAACAATTAGACATCTTGTACGCAAGAGAATTACGATCGGCCATATAAA AACCCCAAAGAGAAGAAAGTGTTTCGAAATTCTCCCAGAAAACAGTCTTATGCCAC CGATTTGTCTTTTCAACATGCATTTGCAATGAAGTCTTTGGATTCTTACTGTGAGTG CTGATCAGCAACGGATTTTCGATCTGTATAGCTCTGCCGATTCCTGGTTAAAGCAG CTAAGAGTTAGGCATCCAGATTTTGAGTTTTTTGCATCTCACAATGTTTGAATACATT TCAAATCCATTGTTGGAGTAACCTAACAACAACTGTACTCTTCTTCCTATTTCTGAA GCCCTCTGCCAGTTTAAGGCAGAGAACTGAGTTATCTACAAGCGGTC
SEQ ID NO:38	Late	LPS-052	GACCGCTTGTATAATAAAGTGGTACCGCGTCCTGCAAACAGGGTTCTCTTGCCATC CTGCTACAACCCTGCAGTGGTCGCAGTAGAGAGAATCGGAGCAACGAACGTTTTC CCGAATATATGGAGCGGGAGGAAGAGTTTTCTTGCTGATGATCCAATCGGAGTCGA ACTGCCACCGCTGGATGAAGGGCGGCGAGGAAATCTTGGGGGGCAGAGGCCCGT CGGCGTAGGAAATAAGAAACGATTTGATATGGAACGAAAGGGCCCGTCCAGGGTT CGATCCCCGGCAGGGCAGCCAGCCCCGAACTAAACAAAACAATAAGAACAAACAG CAAAGTAAAAGAAAGCACCAGAAGAAACAGCAGCAGACGAAGAGTAAGGAGCTGC CCACAAGCGGTC
SEQ ID NO:39	All	LPS-053	GACCGCTTGTAATCCACAGCATTTTCAATAACTTCCTGAGGTGACATCCACCTCCAC TCAGAAAACTCGGCTGCATCTGTCCCATCACCAGCTAGATTGATCTCACTCTCGTC TCCTCTAAATTTTAGGAGGAACCATTTCTGTGCTTGACCTTTCCATTCGCCTCCCCA CAAGCGGTC
SEQ ID NO:40	Middle	LPS-054	GACCGCTTGTATATAATGTGAAGACACAATAAAATTTTGTCCAACAAAGCAACCAAA CGACCAAAAATTTAGCTGTGACATCAAAAAGCTCAACCCCTACAATGAATGTAACCT TAATCTAGAAAATTGATCCATGATCTCCACTGAATTTTCTCGTTCATCCTGAAGAAT GAGAAACTTAAATGTACCCGATTCCCTCAACCAAGCCCCCACAAGCGGTC
SEQ ID NO:41	Early	LPS-055	GACCGCTTGTAATCCACAGCATTTTCAATAACTTCCTGAGGTGACATCCACCTCCAC TCAGAAAACTCGGCTGCATCTGTCCCATCACCAGCTAGATTGATCTCACTCTCGTC TCCTCTAAATTTTAGGAGGAACCTGTAATTGGTAGGGGCTTGTCATAAATGATCAAG ACGACCCGCATCGTGATGCCAAGCTTAGTCTTTCTACTTACTGTCTATGTAATGGTC ACGGGCCCTTCTTATGTTTATGTCTCTTTGAAATGGACGATTTTTTTGTTTTAGGTAT TCAGTTTCTGAAGCTGTTTTGGTAGTAAACTGGGCTCAATCATTTCTGTTGCTTGAA CTTTCCATTCGCCTCCCCCACAAGCGTCAGCCGAATTCTGCAGATATCCATCACCT GGGGGGGCCGCTCGAACATGCATCTAGAAGGCCAATCCCCTATATGAATTCTATTA AATCCCTGGCCTCGTTTTA
SEQ ID NO:42	Early	LPS-056	GGTGCGATCCAGAAAACTATCATCTCTCACTGCTCGTGAACAAAATGCTGGTTCAT AGCCATCACTAAGGCTAAGGTACTATCCAGCCAAACTGATCTCAAATAATAATTTCA TAAGCTTAAATAAATAGTCCAGCCAGTAGATGGAGCCAAAAAGCCATAGAAGCTTC AAATACTTGTGGTATCAATCTCTCCTCTGTTAAGGGAGGTATCAGATCAGAAGCACT AATCAAATGCATACATAAATGCAGTAGACTGCAATAAAACAAAATCTGCAGATAGCA ACAGAGCGCTTAACGAACGGAAAAGAGTTTAACTTGATCTATCACAGGATCGCACC
SEQ ID NO:43	All	LPS-057	GGTGCGATCCACAATAGTTCGTACGAGCGACGTCTATCTGGTTAATCAGAACACAT ATCTAATTTGGAAATTTGTGGGCATAAAGCTCCACAGTGTAGGTGGGCTAATCCCA TGAAACATTACTCTTCAAAACATCATACAACTGAGGTGGAAATTGCAAAAGATTATT ACTGGATGCTGATCTGGGACTAAGGTGGTGGCCATTGGTAATGTTGTGTTTCAGAA ATATATCTTCATGATGATCAGTAGTTGCATCTGGTTGGAAGAATGATAAATTCTGGT AATTTGTCTTGGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:44	Late	LPS-058	GGTGCGATCCAACTAGAAGAATATAAAGAAAAATTACGGACTACCAGAAAACATCA CATCACAGTGTATTGCATTCTCAATAATCAGAACTGTACTGGCTAATATCGCTGTGC CTGTCGTTTCATTTTCCTGTCATCCGCATAGGGCCCCTCATTTTCCCTATCTTGCAG AAATCCAAGAAATGCAAGAAAACCAAAAAGGAAGAAACCCCCAGAGGAAGAGTCCG AAGAGGATATGGGTGTCAGTCTTTTTGACTAGATTGGAGGATCGCACC
SEQ ID NO:45	Early	LPS-059	GGTGCGATCCCAGAACATTTCAGACAGATTAAAACAAGATCTAGTCAATTCCTACAA GGGAAACTTTTGTCAAGATCCGGATCCAGATTTTCCTCAAGTAAAACTAATCTCATT AAATCCAAGCCAATCTCTAGCAAAATTCAAACACTTTTTATTAAATCCAAGCCATATA TCTGGCAAATTCACCGAAATATGTACAATCGCAGCGCATTGCTTGGCTTGCGACAG AAACCATATTCGCACGTCTTCATAAGGCTTTGGATCGCACC
SEQ ID NO:46	All	LPS-060	GGTGCGATCCAACAACACAGCTTCACACTTACTCCATCCTCTGGAACTCTCATCAG ATTGTGTTCTTCGTAGACCAAGTTCCTGTGAGAGTCCACAGGCACACTGAGGCTAC AAGCGATGTGTTCCCTAAAGAACAGGGGATGTACATGTTTTCCAGCATTTGGAATG CAGACGACTGGGCAACCAGGGGTGGGCTTGGGAAGACAAACTGGACTGCCGCTC CATTCAGCGGATCGCACC
SEQ ID NO:47	All	LPS-061	GGTGCGATCCCAACACCAAGTGAGAATGAAGCAATATAAATCAGCAGACTCACTAA AGCCAAAACAGTGAAAAATGTTTCATATTGGGAATCTGCTCCAGAATGAGCCTTCAA GTAAAATGACAAACTAACGAGGAAGAGACATACGGCCATGCCCCCAGATGAGACC ATGAGGAGGAGACGTCGTCCGGCTTTATCCATGAGCCATACAGCAACTGCAGTCAT GATGACCTGGATCGCACC
SEQ ID NO:48	Late	LPS-062	GGTGCGATCCAGGAAATCATCAAAGGGGAGCACATCCAATGTGCAAAATAAGATCA TCATGCAGCAAGATCTCTGAAATATAAGCTCTGTAAGACCAATCTGAAGTGCTGATG ATCAATATGAACTGAAACATCATGCCACAATGGGCTGGTACTTGTGCAAAATTCTCT GGCATGTGATGAGAATCACATGGTTACCTCTTTGGATCGCACC
SEQ ID NO:49	Early	LPS-063	GGTGCGATCCAAAGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATA AATTCCCAGTTTGGAATTCTAAATAAAACTGTTCAATATTTGAAGGCCTCTGATATCA CAGAGACTGATATTAGAATGGAAGCATGTAGCAACCCTAGAAGCTTTCGCATAAAG ATACCAGATTAATTCATAAGAAGGATCTCTCGTTCACCAGTCACATATCACAGTCGG ATCGCACC
SEQ ID NO:50	Late	LPS-064	GGTGCGATCCGTTAGATGAGCTGCCAAGTATGGAATTATTGACATTTTTGGACGGG TTATGGGCAGAGGGATGTGCCAAGCTGAAGAAGATACCGGGGTTGGAGCAAGCCA CAAAACTTCGAGAGTTAGATGTTAGTGGGTGCCCTCAGTTAGATGAGCTGCCAAGT ATGGAATTATTGACATCTTTGGACGGCTTGTGGGCAAAGGGATCGCACC
SEQ ID NO:51	Middle	LPS-065	GGTGCGATCCACATAGTTTGAATGCAAGGAAATTGCACATACTTCGTGGGGAATTT CGATGGCAAATCAGTCCAGGTAAATGACTTCTCAACATAGGTCCAAAACTCTTTCAT AGACCAGATCTTGACCGTGTTGTCCATGCCACAGCTTGCAATACGATATACATCTG AAGGATGAAAATCTACACTGAGAACTTCATTGCGATGTCCCCCAGCTCCAGCAAAT ATCAAAATGCATATTCCAGTTTGAACATTCCAGAGTCGTACAGATTCATCTTTGCTA GCAGATAAAATAAGGGAAGGTTTCAGTTGCTTGGGTCCTTATTTCATTCACAGAACT CCATGGCCAACGAAACTCTTATGGACTTTTCATTTGCACATCCATTCTCGAATTATA CATTGTGACCGCAGCCACTAATAATGGGGAACATCACTCGCCTGCCCACTTATGTG TTAAAGAATC
SEQ ID NO:52	Late	LPS-066	GGTGCGATCCCCTCCATTTACCATGGTATACTGTTCCAAAGGTTCCAGAGCCTAGC TCTTTCAATTCTTCAAGGTCAGCATTCTTTATTATCTGGAAACTTCGCTAGCTGTGT CTATAATCACGAAACCCAGACGGGGAACTAATAGGCGATGAAGTTTCTCTTATCCA TAACCGTTGCAAAGATCTTACACGGAGTTTTCTCTTCTTCTGCGTGGCTTTTCTTTC CCGTATTCTCGGATCGCACC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:53	Late	LPS-067	GGTGCGATCCATACATGCGAGGGCGCATGAGAGACTACCACAAATCCTACATACCT CCATTCACCCCTGGATCGGTTATACAAGGATTTGGGGTGGCTAAAGTGATACTCTC AAATCACCCAGACTTCAGAGAGGGTGACTTTGTATCTGGTACTATAGGATGGGAAG AGTACAGCATAATACCAAAAGGGAGTAACTTAAGAAAGATCAAATATACGGACGTAC CACTTTCATATTTTGTGGGTGTTTTAAGAATGCCCGGGTTTACTGCTTATGCTGGAT TCTTTGAAGTTTGCTCTCCTAAAAAGGGGGAGCATGTTTTTGTCTCTGCCGCTTCA GGAGCTGTTGGCCAGCTTGTTGGGCACTTTGCAAAGTTGATGGGTTGCTATGTTGT TAGGGAGCGCGGGTAACAAACAGAAGGCTGATCTGCTGAAACATAAAATGGGCTTT GATGATGATCTCCACCATAACGAGGAGCATGACTTCGATGTGGCTTTAAAAAGGCA TTTTCCAGATGGGATTGCACC
SEQ ID NO:54	Late	LPS-069	GGTGCGATCGAACTGAATGAATGACGTTGCCAAGCTATGTTTGGGAATTAAAACTT GAATGCCGTTATTCTCTCCTTTTTCCAAAAGGGCCTTTTCTGCCAGAAAACCTTAAA TTTCTGACTGGTTTCCAAGTCCAATTTTTAAAATATGGATTGGTTTACCATTGAAGG CACCACCATGCTCTGAAAGTTATGGACTGCACTTGCCCCAGTGCTATATTTAGTCC AGATAGCGCTTGTGTCTCTAAATGCATCTCCCTGCTCGGATATCACC
SEQ ID NO:55	Late	LPS-070	GGTGCGATCCGAACAGAGGGAGCAGATTTTGCCCTTGCAAGTATTCACAACATTAG AGAAGCCCTGCCAGAGATATGGGAGGAAGAAGATGCAGAGAACACCAAAAATGTT GTGGGATCAAGAGGAGCGGATGCAACTATAGAAACTGTTGTCACGGCATAAGCCA TCGCCTCATTGAATGAGGGAATGGAGGACTAGACAAATCCCTTTGGATCGCACC
SEQ ID NO:56	Middle	LPS-071	GGTGCGATCCGATTGGGCAGCTGCAGCCTTGGGAAGCTTTAGAATCAAATTGCAC TCATCCTCCAGGAGGTATTGAGAAGTCAATTTCTCAAGGTCTACAGTGACAGAAGG AACCATCTTGACAATCTTATCAGGTTTCCTGCTCTGGTTAAACACTTCAACTTTGAC AGGACGAGAGAATGTGACTAATTCATCTTCTTCATCAGACTCTACATCTTCCTGTTT CAAGAAACAAAGATACTGATCATCACTAGGGCAAGAATTGATGATTTTGATATCTCT GGAGAAGCCAGTGTTTACATTGGTTTGCTTCATGGCCACCAGTCTATGGCATAAAG CTTTCCCGAAAGGGTACTTGGCAGATTTAACAGAGCCCAACGTTATATTTAAGGCC CATCTCTTTGCTCTCAAAATTTTTCTTGCATCCTCTGGAGAATATAAAACCCCTTGG TGTCTCTTTCCACAAACACCTTCTCATTGATC
SEQ ID NO:57	Late	LPS-072	GGTGCGATCCAACTGAGAAGGGTGTTTGGTGGAAAGATGACACCAAGTGGGTTCT ATATTCTCCAGAGGATGCAAGAAAAATTTTGAGAGAAAGAAGATGGGCCCTTAAATA TAACGTGGGGTTCTGTTAAATCTGCCAAGTACCCTTCAGGAAAGTTTATGCCATAG ACTTGGTGGCCATGAAGCAAACCAATGTAAACACTGGTTCTCCAGAGATATCAAAA TCATCAATTCTTGCCCTAGTGATGATCAGGAAGATGTAGAGTCTGATGAAGAAGAT GAATTAGTCACATTCTCTCGTCCTGTCAAAGTTGAAGTGCTTAACCAGAGCAGGAA ACCTGATAAGATTGTCAAGATGGTTCCTTCTGTCACTGTAGACCTTGAGAAATTGAC TTCTCAATACCTCCTGGAGGATGAGTGCAATTTGATTCTAAAGCTTCCCAAGGCTG CAGCTGCCCAATCGGATCGCACC
SEQ ID NO:58	Late	LPS-073	GGTGCGATCCATGTAGTGCCAACTTACGAGATCACTAACTTTAAAACTATCATGCAA TTGGCCAATAGAAGCGACACTTGCTGTGCCAAAGTATCGATAGGCTACTCCCGATG GCTCAATCATATATAGTTGGGGCCCATCTCTATCATAACCTCCAAGGATAACTCCAG ATCCAAAAGGCCTTAACCACCAATATAGTGTGCACAAATGCACATAACTGGCAACA CGTTCACAAAGTTCCTTAAT
SEQ ID NO:59	All	LPS-074	GGTGCGATCCCATGGGATAGTTGCAAGACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTAGCAAAATTCAAACACTTTTTATTAAATCCAAGCCATATATCTGGCAAATTCACCG AAATATGTACAATCGCAGCGCATTGCTTGGCTTGCGACAGAAACCATATTCGCACG TCTTCATAAGGCTTTGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:60	Early	LPS-075	GGTGCGATCCCACTGTAGTTGTCCTTGTTGAGCATAGTTCAAGCTGTTCTGATTCC ACCAGTTAGTGGCCCAACACTGCGAGGTGCTGCCATTTCCATTCCATTCACAGACG TCAGTGTTGAAATTCATATAGGAAGCCACAAAGGGTGAGGAAGACCAATCTATTTTC ACTCGCCCCCCTTGAGTTGCCCACTGGTCTCCGCTCCATATGCTAGAGAATACTCT CATTGCCTGCTCATTCGGATAGGGAACGCCTATGTTTTCATTGTTTGCAAATACTCT GATTGGCAAACCATCAACGAAAATCGCAATTTGCTGGGGGTTCCAGAGAATAGAGT AATTGTGGAAATCTGCTGTAGGATCGCACC
SEQ ID NO:61	Early	LPS-076	GGTGCGATCCCACACTCCTAACCCTATTATATGTCTCCCGTCCATGGAGTCATAGA AGGAGTACGATAATATGCCCTTCAGCCAAGCGAAGTATGACTTTAGTATGGCCAGG CAGCAGTATGAAAGCACATCTTGTTTCTTCCAGGTCGGCATGTATAGTCTCCGGAG GCTAACAATGTCACCCAAAGCTAATTGCGCAAACGGAACTCCTCTGCTGATCTCCC GGGAACTTAGGCGGAACCACCCTGAATCCACTATTCTCACCGCGCATTTCATCCCT TTGGTGAACGCCGCTGCCTCTGGTAGATACAGAGCTGGCTTGTCTCCACTGGAAC CCCCTTTCCGGATCGCACC
SEQ ID NO:62	All	LPS-077	GGTGCGATCCAAACTGTGGTTATCGGTGGAGAGATTAAGCAATTTATTGGAGTAGC AAGTACGCTGAATTAAGGGGGTCCATCTTCAAGCAAAGGTTCCTTTGGATGACTAT GTGTTCTGGAAGTGTTTATGGATCAATCATCTCATAAATTTTGGTAATATATAACAGA AGATTATGGCATCCAGTTAGGATGGTAGTTTCATTGAGGTATAGTAAAAACTACACT AGTCTTGTGTTGCCACCCACTTTTCAGAGAAGTCAGGAGGTCTCTTTGTGAATCATT GATAACTTTATGAGTGGGTACCTAAATGAAATATTTGCATCTTGAGTATATACTCAAT TGATCTTACTTGTGGATCGCAC
SEQ ID NO:63	Middle	LPS-078	CTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTTACG GCTGCGAGAAGACGACAGAACACCTATCATAACTTGAATTCTGATGCAAATCGGAA TTTGCCAAAAACTTGGACGGAAATATAATAGGCAATATCATCCCCGCAAGTAACAAA AAAATTGCATGAAAGCTCAAATCCTATGTGCTTTACACCTTGACTGCATACTTTCTC ATTGGAAAATACATCTCTTTCTTTTTCTGTCTCTCAGTCTTCAATGACGCCTGATGCT TGGTAAGGCGTCGCCTGATAGCACGAGTCTTCTTGGGACGCAAATCAAGAGGCAG GTACTTCTTTTTTTTGTATGCTTCTCTTAATGCGGATCGCACC
SEQ ID NO:64	Late	LPS-079	GGTGCGATCCAAGATTGTACGGCACAGGCAAATGCTGTTCTTTTTCTTAATCACGA TGTGCTTGAAGAATATGAGCGCCGATGTGAACAGATCCACAACCTGGAGTTAAAAT TGGAGGAAGACAGAGCAGTGCTGAATAGGAGCTTGGCAGAAATAAATAGTCTTAAG GAATCCTGGCTTCCCACATTGAGGAGTTTGGTTACCAGAATTAATGAAACTTTCAGC CACAACTTTCAAGGGATGGCTGTTGCTGGAGAAGTTACACTAGATGAACATGGCAT GGATTTTGACAAGTTATGGTATTCTAATAAAAGTCAAGTTCAGGCAAACTGGACAGT TGCAGGTATTGAATTGCTCATCATCAGTCTGGAGGGATCGCACC
SEQ ID NO:65	All	LPS-080	GGTGCGATCCGAGGGAAGCGATGTAGTCTTGCCCCAAGCGACGACCATGATCCCT TATTCTTGGGCAATATGTGCAAGACGTGGACAAATGAAGCGGTTAAAGGGAAGCTT ATGGACTATGGAATAGAGGGTCTTGAAGAGCTAACTCTAGTGGGTGATACTCAAAA TGAAGGAATAAGCCGTGGTTTTGCATTTATAGCATTTTCTACGCACATGGATGCGAT GAATGCATACAAACGCCTTCAGAGGCCAGATGTTATTTTTGGTGCTGATCGAACTG CGAATGTGGCATTTGCAGAGCCACTGCGTGAGCCTGACGAAGAGATCATGGCCCA GGTTAAGTCAGTGTTGTTGATGGGATCGCACC
SEQ ID NO:66	Late	LPS-081	GGTGCGATCCAGTCCTGAAAATGTACTTTACCATTTGTATAATGATGTAAAAATCTT GGCCATAGTCTGGTCAAACCAGACTGTATTGTTGCTAAAGTTATGGAAATTCTGGC CATATTTTTGTCTAACCAGACTGTATTGTTGCCAAAGTTATGGGAATTCCGGCTATA TTTTTGTCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATCATAGGG TTGTCTGTGCGTGTCTCTCTTCTTACACAACAAATTTGTGTGTTTTGCAACTATCCC ATGGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:67	Early	LPS-083	GGTGCGATCCGCTGGAAGGTGGGCAGCTGGACATCTGGGAATTATAAGTCGAATG TCAATTGCTGGGCCATCTGGGGGATGAGCAATAGCATCGGAGGCCAAGTTCTTCT GCAGCCGGGCACCAAATGCCATGTGGAGGTCTGAATCTTAGTTTGGAGGTCGAAG TTTCAATCCCCTTGTGTTTACTCTGTTTCTGGTTTTATTTGAATAATTTGAGCAATTT AATGTGGGTCCTTAGTGCTTCTGTGGATCAGATTCTAGGGAACGCCATCCTGATAA GTAAAGATCCGAGTTTTAATGGAGATTCAATTCTATCAGAATTCCATGGTGGTTTAA ATTCCCTTGTACTGTTGATCTACGTCGCTTTGTATATCAGTGTGTGTTAAGATTTTCT CAGAATCCACAGCTTTGTTATGGATCGCACC
SEQ ID NO:68	Middle	LPS-084	GGTGCGATCCAAGCACTTACGACTCCCAACAAGGACGGGAAACTCTAAAATCGGAA AAATATCATATACTGAGGCATCAACTTTGTTGATAAAACTTTAAACAAGAACAATATT TGCAGCATATTAGCCCACATGCCATAATGACAAACAAATATGAGAACACTGCCTACA GGTTTGCCAAAAGCATGGCCCTCACTTTTGCCCTGAGGTCATCAGGAGCTTCTGAG GCTCGAGAAGGAGAAAAAGATTGTGTCACTTCAGGAGCTGAGGCCTCCACATCTTT TAATGATTTCGCAGCAGGCCTCTCTTTAATGTTTTCTTTAGAGGATCGCACC
SEQ ID NO:69	Early	LPS-086	GGTGCGATCCAAGGTACGAGCGAACAAGTTTCTTCAGCAAGCCACCTGGAACTTTC CATGAGTCCAAAACAAGTTGAAGAAGGCTTCTTTGGCTACTTTTAAGATGCTGAAGT GATTGTGCTCGCCTCTTGCACAGTTCAACCGCAATAACATTGGGTTTTACAAAACC GATTACCTGTTTAACCTGCTGTGCACTCTTTTTCGAAACATGACAAGTTCCAACAAG ATAAACTTCGGCCCCATTCTCGCCATTCCGCAAATAAACCACGCTCTCATCTTCTGT TATCGAACTCGAGTGCATGCCACGACGCTCAATTGCAGGATTCCAACCCCGGACTT GCGAATGGTGCAAAGCGATGCCCGTTCGTCTCAGCGATACTGCTAAAGATCGGCA GACCCGAACCAGTTTGATGCTTCCATTGCCTTAAACATCCAGAGTTTTCCTTCGACC TTAAACCCTAACAAGATTACTGATTTCTGGTCCGGATGTTCACTGTCTGTTATACTT CTCACAAATCTGTCACACTCCTGATAATCTTCGGTATTGAACTTCATTGAATTGAATT TTCCTTCTCATTGGAATTCAATTGTACCTTGTAAATGTCTGGATCCTACACTATACCA ATATTTACAGGTCTGAGTATTTTGCCTGTAGTATAATTATCTTTCCTTCGGTCTCGT GTTTCCGTATTATTCGTGTAGGATCGCACC
SEQ ID NO:70	Late	LPS-087	GGTGCGATCCCGGGGGGAGGTTGATGTTCTGAGAGAATCAATGAAGGGATTTCAG CTGAGCTTGCCTTTTTGAAGACGGAATGCGAACAACCAGTCATTTGCAATAGCGAG AATTCTCTTAAGCCACTGCCTGCTGGGGAGGCGAGTTCTGATTCCGGTGATTGCAT CACTCAACGGCAGCAGCAGCGGCAGAACCTTTAGTTTCCCATGACAGGTCTCTCTG TACAAGTATCTTCCTGTTATGATCTAATTCCGGGTTGTTCGATTATCGTGATGTCTC CTGTATTGACATATTAGCAGAATATTACCATGATACGATGTTAAGTGGCATGGTTTA TGCCCTGCATGTTATGTTATGGAGGAGGTGAGGCATGTGGCGCTCATGGGAGGGC CCACATGGTCCATGGACGTCTTATTAAACGCATAGTCGTGAATGAAAATAGTTCAAT ACATTCAAAATTCCAACACAATTTCATTACAATGGAAGTGACTTCGACTTGAATGTT CATTGAAGCATTTGCATGCACAAACAAAGTATACTAGATTAGAAGAAAATTGCAAAA AAGGACATTGTGCCCTTCTTAGTGAATATATAAAGATGTTCTTCATGCTGGATCGCA CC
SEQ ID NO:71	Middle	LPS-088	GGTGCGATCCCAATAGCCAATATTGCCTCCAAGATAGCCTAGACTGCCTTTTGCAT AGTTCTAGAAGCCAGTCACCCAACCTCCCAAAAGAAATTGCGCAATCTTTCCCATC AGTTTCCCGGGTATGTGTTCTGTCATTCCCCGAATTTTCTTTGGTTTTCACTAATAG ATTTCTTTCCATGCACATTGCTTGTCTCCAGATCTTTTAGGTGTTCATCCATCTCTTA GTAGTACTAGATCGATGGCTTCCAAGAGAACAGGATCATATGACACTGTTGGAAAT GTAGCTGGAGCAGCAGTTGAGCAAGTGTCCTCTAGTCTATCTATCTATGAAAGATA CACATTGTTTCTAGACATGGATATCAAATTGAAATTGCCAGAAGTCCATGAAACATT TGCCGCCTTTTGAAGAAAGGCTCCAAACTGTCAGGGTTCGTTGAACATCACATGTT CTCGCTGTCTGATCCCCCC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:72	Middle	LPS-089	GGTGCGATCCTCAGGGTAATGGCCTGGCTGAATCAAGTAACAAGAATCTTATAACC ATTATCTAAGAAGATAGTAGGAGATAACAAGCGGTCTTGGGACAACAAAATCAAGT GCGCTTTGTGGGCAGATAGGATAACTAAAAAGAAAGCCACTGGTAAAAGTCCCTTT GAACTTGTCTATGGCATGGATTTGACATTACATGCCCATCTTAAATTACTAGCTTAC CAACTCCTTCAACATTTTTCTAGTGATAAAGGTGTTGTCCAAAACATGGTTGATCAA ATTGTGCAGTTGGATGAAATCCGCAGGAAAGATTTTGATAGTGCAAAAATCAGTCTA CCATTAAGAAAATCTTTGACAAATCTTCTCGGTCTAGATATTTACAGGTTGGAGATA TGGTTTTACTATGGATTCCACC
SEQ ID NO:73	Late	LPS-090	GGTGCGATCCTGCAGGCTTAGATAGTTTCGGCGCTCCTCTGAAAGAAGCACGAGT AGGTGTCTCCACATTAGGTTGGCCTGATCCCTTGCCTGCACTTGCAGCTTGTCTTA CAACATCTCCTATGCTTTGATCCAGGCTTTTCACTGACATAACTTCAGGGGCTTCCT TCTCCCAGGGCCGTGCTGCCATCCAGCGTTCTAGCCAGCTCCATCCCCAATTTGG CTTGTTTGGGTCAATTTCCATCAGCATAGGATGAGCTGCTCCTCGTGTGCTTTTCAA TGACTGATGAGAATATGCGTTATGCCAATGCCCTTTCTCGCTTCATGGCTGCTTCTT GCTTGCTTTGCAAACTAGCCTCAATTTCCTCTTTGGATTGCAACTGTCATCCAATCC TTTGCTTCCATACTGGATCCAC
SEQ ID NO:74	Late	LPS-091	GGTGCGATCCCAAATGAACATTCAACATTCGATCATGTCAAGCGCTAAATGCCTTG GCAGCTTAAAAGCTAGACTCCGCAAGTGACCCTTCTGACTTAGTACACATATTAAGA CTCATCAAGGGTCCAATTCCATGAAAAGAAATTTTAAAACGGTTACATATTCACAAG AACAGCACGAGATTTCCCAGATAGTCAACCACCAACTTGCCCTATCAGCCCAAATA TTACTCATTCCATGTTAAAAATAGCAAATTTCCAGATAGAATGTCGAAAGAGATCTT CATGCACCATATATGGACTCTTAAAACCAGCCAAAATCTATACTGCCATGCTTGGAT CGCACC
SEQ ID NO:75	Late	LPS-092	GGTGCGATCCTGGAGAGAGAAGCAAAAAGCCTACCATCTAAATCTACATTCTAAAT CAGATATCTTTACTGTGAAAGGAATTGAATGCTGCTTCAGATATCCTACAAGAATTA AGAAGAAAAGAATGATCAACTCCAAATCAGGCAGATGGCTCAGAATTTCCCGCAGC TTCATTTTCGACGGCCTCCACAACACCAACCTCGGCAGGACGTATTACTCTGCCAT GAAGTGTATAGCCAGGCTTCAAAACCACAGCCACACTGCCAGGCTGCTTACTAGCA TCTTGAACTTGAGATACTGCCATGTTGCATATGAGGATCAAACTCTTCATTTATTGG ATCGCACC
SEQ ID NO:76	Late	LPS-093	GGTGCGATCCCCAGAGGTTATTTTGGGTTCAAAGTATTCTACACCAGTTGACATGT GGTCATTTGCTTGCATAATTTTTGAACTGGCTACAGGTGATATGTTATTTGATCCTC AGAGTGCAGAAGGTTATGACCGCGATGAGGACCACCTTGCCCTGATGATGGAGCT TCTTGGAAAAATACCTCGTAAGATCGCCTTAGGTGGGAGCTATTCACGGGAACTTT TTGACAGGCATGGGGATTTAAAGCACATTAGACGGCTTCGGTATTGGCCCTTGGAT CGCACC
SEQ ID NO:77	Late	LPS-094	GGTGCGATCCTAAACTGTATGTCTCCACAATTGTCTTCAATATAGAAGCAGCTACG CCCCTCCTAAGTCATCATAAGTTAAAAACTTCATCTTTCCAATACAATTAAACTATCT AGCTTATCAGTTTGGAATAGAGATACAAAATTACAGATAGATTAGCGAAACTGTGCC ACAAAACCTCTTCAAAATTAGAAGCATGATTGTCTACAACTCCACTTCAAAAAGGAG CTGAACCAGTCCTTCGAAGGGTGTGCTTTGGTTGTGGTGGAGGTACAGAAGGCAG CAATTTCTCCAAGAACTGCTGTTTTTTTAGCCTCTCATTCTCCTCTTTAAGCTGCATC ACTTCATTCTCTAGCTCATTTGTGTATGCCTGCTTTCTTGCCCTGGATCGCACC
SEQ ID NO:78	Middle	LPS-095	GGTGCGATCCGAGTGATGGCACAAAGAAAAGCAATGATAGAAAACAAAGAACAGGT AGCTCAGAAGGTTCAGCAACTTAGAGAGTCAACTTCGAGTTAAGGAGGGCGGGAG CAATTGGCAGATTCTTCCAAATTTGTCAAGATCTCTTGGCATGAGATGACCTTATAG GATGTTAAGGAGCAAGAGGATTCTAGGAATAATGCCAAGGATAATAAGACTAAAAG GATGCTTCAAGACCAGGTGGCAAGGAAGGCTTCTAATTCAAAGGGAGTTAGCAAC GGCAACAGATGCAATTCTAGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:79	Middle	LPS-096	GGTGCGATCCTAGAATTGCATCTGTTGCCGTTGCTACTCCCTTTGAATTAGAAGCC TTCCTTGCCACCTGGTCTTGAAGCATCCTTTTAGTCTTATTATCCTTGGCATTATTC CTAGAATCCTCTTGCTCCTTAACATCCTATAAGGTCATCTCATGCCAAGAGATCTTG ACAAATTTGGAAGAATCTGCCAATTGCTCCCGCCCTCCTTAACTCGAAGTTGACTCT CTAAGTTGCTGAACCTTCTGAGCTACCTGTTCTTTGTTTTCTATCATTGCTTTTCTTT GTGCCATCACTCGGATCGCACC
SEQ ID NO:80	Middle	LPZ-001	ATCTAGATCATCGATCTTGTCCAAATTTTAACTAGTGAATAGTTTTAAAAAAAAGCAA CTAGCAGAAGAGAACCTAACCACTGACAAATTGCAAATACTCTAGAACACTATTCAT CATTTTTTGCGATTCACGCTGGACCCACAAGAACCCCTTGAGCTGAACTTTCTTTTC GTTCTCCCTCCTTTTGGATCGCACCATCTAGACCATCGATCTTGTCCAAATTTTAAC TAGTGAATAGTTTTAAAAAAAAGCAACTAGCAGAAGAGAACTAACCACTGACAAATT GCAAATACTCTAGAACACTATTCATCATTTTTTGCGATTCACGCTGGACCACAAGAA CTCTTGAGCTGAATTTCTTTTCGTCTCCTCCTTTTGGATTGGACATCNAATCCTGCA GCCGGGGATTCATATTCTTAACGGCGCNCGCGNGGACTCCATNCCCCATATGATC TTTTCATCCTGGCGCNTTTAACTCTGAAGGGAAACCGGNTTNCCCTTATCCCTGGA NATCCCTTCC
SEQ ID NO:81	Middle	LPZ-002	GTGGAGTGTAAAGGTCAACGTGCCATCCGGGTACAAACTATTGTAGAAAAAATGGC AAAGTTAGGTCTGAAAATATCCATTTGGCCTGCTCTAGTTGTACAGTACATGATTTT GCACTCGCACAACAATGGACTATAATTATTTTCCTGGCAAAAAAAAAAAA
SEQ ID NO:82	Late	LPZ-003	GGTGCGATCCAGGACATGAGGCCGAGTTTGCCATTGTGATATGATTGAGGAAGTC CAGTCCTAAAATTAGGTTTATCTTGATGTTTGACAAGAGATATAGAGGGGCATGATG ATTCATTGATCTGTTTGCAGATCTGTAACTGCAACCATTCTAATGACATAATAGCGC TATTGTTTGGGTTCGTGTGATGACATAATAAATTGATTTAATTTAATAACATCTGTTA ATGCAATGGCTGTAGCTGCATCATCACCGTATCCATCGAATGTTCCATTTTTCCAAA TGTTTGTTTCCAAAACCAGAACACCAAAATGTCCCCTGCGTTTGTNTTGAAAAATAT TGGGCCCNTACTATACTATAATNTTTNGGCATACTATACTATAATGTTTCTCCCATTC CCCCCAAATGANTCCTATACAATCCTGGCCGNCTTTACACTCCTGACNGGAAACCC GGCTTNCCACTAATCCCTGGNCNANCCCTTC
SEQ ID NO:83	Late	LPZ-004	GGTGCGATCCGACTGTGATATGTGACTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTTTAGGGTTGCTACATGCTCTCCTCTTTTGTAT GAATTTCCATTCTAATATCAGTCTCTGTGAT
SEQ ID NO:84	M,L	LPZ-005	GGGGAGTGTCAAGGGATAAGTGGTAAGCCAGGTTTCCAGTCAGAAGTGTAAAGGC GGCCAGTGATGTAATAGATTCATATAGGGGAATGGAGTCACCGGGGTGCGCCGTT TTAGAATAGTGGATCCCCGGCTGCAGGATTTGATGGTGCGATCCTGCCCCTGATAA TTTGGTTGCAATGGAAAATGCAGTATTAGGTGCGAGATGTAAAGCCCGCCCGGAG CGGTGCATGAAGTACTGCAATATTTGTTGTAGTAAATGTGCTGGTTGTGTTCCCAG CGGTCACTATGGCAACAAGGACGAGTGCCCCTGCTACAGAGATATGAAGTCCGCA GCCGGCAAGCCCAAGTGTCCCTGATCTTAGCACTTCAGTCCAGTCGCTCACTTCTT TTATTCTTTTTTTTTATAAAAGTGACGAGGCCGTTTTTCTTGTACTTGGTGGCCATAT GTAGAGCGGTGGCTACTTCTCCTGTGTTAGGAAATGTTGCAGTACTAATAATAAGA ACTTCTTTGGCAAAAAAAAAAAA
SEQ ID NO:85	M,L	LPZ-006	GGGTTTCCTTAAGAGTTAAAGGCGCATGATGTATAGAATCATATAGGGGATGGATT CCCCCCGGGGGGCCTTTCAGAATAGGGATTCCCGGCTGCAGGATTGATAGTGCGA TCCAAGACACAGTGGAGTACCACAATGGGGATCTGGCCAGTGCTTTGTGGCTATTC ACTGCAGCTGTATTAAAACAGGAAGCCGCAAATGGCCAGAAGGCCATTGAACTTGC TGAGAGCAGACTATCTAAGGATGGCTGGCCTGAATATTATGATGGGAAGCTTGGAC GATATATTGGAAAGCAGTCTCGAAAGTGGCAAACCTGGTCAGTTGCTGGATATCTT GTAGCCAAGATGATGCTTGAAGATCCATCCCATTTAGGTATGATAGCATTGGAAGA GGACAAAAAGATGAAGCCGTCCCTCACTCGATCAGCTTCTTGGATAATGTAAAATG GGGAAATCCTAAACTTTCAGGCCACTCTTGAATGTTTTGTCACTTCTGTATGACAAA TGAGGCAATTCATAGTACATGTTGTGCAAAAAAAAAAAA

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:86	M,L	LPZ-007	GGTGCGATCCCAGAGAATATTAGTTCATGTGTTGCTCTCATTTTCTTCAATATGCAG GGCAACCATTTGAATGAAATTATTCCTTTCGAATTTCAAAAACTTAATAGGCTAACTT ATCTATCTGGAGCCGATTTTCATTGACGAGTAACCTGTAAGCTGGCCAGCAAAAGC CAACAGATGTTCAGCTCGTTGGAACCAGTTGAAGATTGTAATAGAGATGGTGAATA ATCGCGGACGGCTCGGCCAATGGAATATTTGTTGCATCATCATCAAGGGGGTATGA ATTCCAAAGAACTTGTTGATTGAAATTCCCAAGCAAAATTCTGTGAAATGAAAAATTT ATTGAGACCATTGGGCAAAAAAAAAAAAA
SEQ ID NO:87	Late	LPZ-008	GGTGCGATCCAAAGAACACAAGATGGAGTTACCACAATGGAGGATCTTGGCCAGT GCTTTTGTGGCTATTCACTGCAGCCTGTATTAAAACAGGAAGGCCGCAAATGGCCA GAAGGGCCATTGAACTTGCTGAGAGCAGACTATCTAAGGATGGCTGGCCTGAATAT TATGATGGGAAGCTTGGACGATATATTGGAAAGCAGTCTCGAAAGTGGCAAACCTG GTCAGTTGCTGGAT
SEQ ID NO:88	Late	LPZ-009	GGTGCGATCTGTGTGGCTCTGAAACATCCCGGCTCCCCTCTGCACTATAATAATCC CAAAATTAAGTGAACCCAACAGAATTTGCTCATATCTCTACAGTTATTGCAGACTGA GCAAAACCCTCAAACTCATGTGACCTCTCAATAGGAGCCCACGCCCAAGATTTGTC CAGCATGTAACACACCTGATCGCCGCCACTGCAAGCACAACCGCTCACAAATATCT TGTCACACCACACTGTTGCGCAAGTTAACAATATTCATGTCTCCAGGAAAGAAATGC CACACTTCCCAACATTCTCTTTACTATTATAGAACTTCCTTGTTGCTATGGAAAAAAT ACATTCCCAACGCAGAACCCCAACGGGGGTTCCCAATANCCCATTTCCCCCCTNTC CAANCCNNTNTGAATGCNCCCCATNCCCTATTGNATNNTTTAAATCCNGGCGCNTT ANCTGGAAGGNAACCCGNTTCCCN
SEQ ID NO:89	M,L	LPZ-010	GTTTTCCCAGTCAGGACGTGTAAAACGACGGCCAGGGATTGTAATACGATTCACTA TAGGCGAATTGGAGGTCGATCCGTATAGGTAGTTGGATGATGAACGGGCAAAGAA GGCAAAGGAGTACAGTGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCT GCAATATAAGGATGGCTAAGCTTTTCAGCTATGAAAATATATGGTGCAGTGGCACT CATATCAGTTGCAGAGTTGTCAATATAACTTTTGTGAATAGGAAAGTTGTCCTCTTT TAGAGTGCAGAAATCCTGCAATATAAGGATGGCTAAGTTTTTCAGCTATATGAAAAT ATATGGTGCAGTGGCAAAAAAAAAAAA
SEQ ID NO:90	All	LPZ-011	GGTGCGATCCTACAGAGAGCAGCTTGACGAGGGCCAAAAGGTTAAGGATGAAGAA TGACCTCAGCTAGTAAGGTTTACAGAAGCAGCAGAGGCATCTTAACTGTTTTTATGT TTTGGCAAAAGTTGTTGCGTCGGTTGTTTAATCCAGGATTTCAGATGTATTTTGTAG A
SEQ ID NO:91	Late	LPZ-012	ATTGTAATACGACTCACTATAGGGCGAATTGGAGGGTCCGATCCTGCGAGACCGA GGGTTCATTTTCCTTTAGACAACGACGTTCAGTGGCGACCAGAGTTTCCCAATCAC TTCAGCGATTCTATTCCTTCGTTGTAATAAAGCTTAAGGAATCCATGCTTTATTCCTT GGAAGGTTTGAATATTTATATTTATTGGCAAAAAAAAAAAA
SEQ ID NO:92	Late	LPZ-013	AGGTGACCGTCAAAATGATTGCAGAGGACTTAGAGAGGGAAAACCGTTCCGATCT GGTGAAGCAATTGGATGAAGCAGCTCTGGAATTGATTCCCGTTTCTGATGATATCG TACGGCTAAGCTCAGCTCTTCAGGCAATTGGCAGAGAATACGATTCTTCAAATGAG ATGACAGATTTTAAGAAACTTATAGATGAACATATTTCCAAGCTTGAAGCGGATTCC CCTACGGTCACCT
SEQ ID NO:93	Late	LPZ-015	AGGTGACCGTAAAATACTATGAGAAATGCTTTCATCAGGCACCGCTGGTAGGTTTT CTTCAAGCTTTTCATTAGGCAAAAGAGGCTCCGTGAGTTGATCGTTAATTCTCTCCT TGAATGGCCATATTGACCAGACACTCTGATTAGAAACTGGAATACAACTGCACATAT AGTCATTCTTATATGATTCATCCTTCTGCACTTCAGCATCCTGCGGCAACTCTTCAT CCCGCCATACTGCAGAAAAATTATTTGACTCTTGATCATGTTGTAGATGAATCTTCA TGAATCTTCTCATCTTGCATTCTTGTCTTTATATCTTTAGGAAATTGCATCTGGTAAA AGTATAAATGCATCTTCACTGGTTGCTTCAGTTTTTGCATGCTCCTGTTCTTCTTGTT TACATGTGATCTACCAAATCATCTAATGTATTCTCTCAATGTCTTGTGGACATTCTCC TTCATTCCGAGATTACCAATCATCTACCCGAATAAATGTTGCCCCGTCAGCAATGCC GTTTTGGTCC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:94	Late	LPZ-016	AGGTGACCGTAGTAGGCGTCCAGAGGCTGACAAAATCCCAGGCCTGTGCAAATCT GGAAGCCGCATGCAGGGCCGTGGCACCTTACACTTGCGGCCTTAACAAAGTGGCC CGCGGCACCCACTTCTACCAGTGTGTTTATATTCTTGTGCAGCCAACACCAGAGGT TATGCAGGCGAATGTGCTGGCCAAGCGTTGTTTCGGCTTGTCCGCAAACCCTCTC GAGTCTTACATGCCGCATATGAGTCTTGTGTATGGCGATTTGCCTGACGACGAGAA AGAGAAGGCCAAGGTTAAGGCGCAGCTAAATTCGATGAACTTATCCGCAACACGGA ATTCCAAGTCTCCAGCTTGTGCTTGTACTCGACAGATCTGAAAATAATCCTCACTCA TGCATAAGTGCAAAATGTGATCTTAACCTGCTCTGAAAATTACATAA
SEQ ID NO:95	Late	LPZ-017	AGGTGACCGTCCACGAGAATTTGGCTTCAAAACCCTAGGAGAGGGATATGAACTTG CCAAGGCACAACTGACGCATGAACAAGACGTAAAATGACTCATTAGACACTGACAT GATAATGAAAAACCTATGAATGATGATAGACTCAGCTACTTGATGACATCGCCCGC CATTTGGACATCTTTATAAGGAGTTTAAGCAAACCCTAGACCTACTGCCTAGTGACC AACTTTTGCTTGACGACTCACTGAAATGACAATATTTGACCTTGACACTTCAAAATC ACTTTGTAGGAACTCATTTGATCACTGGAGGACGGCTGGAAAGACTGACACTAACA GGACTTTATATATGCACCTCGTCTATCCGAACTT
SEQ ID NO:96	Late	LPZ-018	AGGTGACCGTAAGCACAAGTCGTCAAAATTATCTCTATTCCGGCAGTAAAAACCTAT AGCTAATGATGGATCAATAGCACTAAGTGGCAGCTGGCGTACATCACTGCAATGAT AAGAACCAGTATCAACCCCCATATTATCAGGAGATATCTCCACCACCTGCTGCACT ACATGTGGATCTAAGTACAGAGCCTGATCATCCTGAACACCAACAATATACGTTGAA GCTCCAGGCTTTCCACCAGCAATACCAAGACTTTGGGGAAATGTGAACGTTTCACG AAGTGATGGTACATACCTTGGGTTGATCTTCTCTACACCAAGAACAAGCGGCACCA AAATCAGGATAGGCACTTGGTCTTCCCCTTCTCCATTGGACCACTCTGAACACAGC CTCGCAGCATCATCAATGCAGATAACTGGAGTCCCTCCACGGTCACCT
SEQ ID NO:97	Middle	LPZ-019	AGGTGACCGTGAATATGGTGGGTATTTGCAGGGCAAGATTCAGGATGCTGCTCCC GGAGCTTAAGTAAGGTCTTGGACCCTAATAAATTCAGGGTATATGCATTATGTATAT GCTCTCATTTAGCTGCTCATCTGATTTCCATTGGGTGAATCAGTTGTTTTGCAGTAC GTGGGGGTCTGTTTATTTTGTGAGTTTATGGTGGAGTTCATTTTGTTGTTGTTGTTT TTTCTTATCTAGGGTTTAGGGTTTTGCCCTGTAATCGGTCTTCCCCTCTCTCCTGCG CTTGAATTTGACCTGAAACCTCTTGAAGTAGGCCCTGGTTTTCTGGGCTTTGACGA AAACCATGGTTGTGGATCTCCTCTCTCCTGCTACGGTCACCT
SEQ ID NO:98	Late	LPZ-020	AGGTGACCGTCCTACTTCACCGCAGTGACTTCCATCTGGTTTTAGGAAACTATCCC TAAATCCTTCACTAGTTGACGAATTGATTGACTCAAATCAACTGTCGGTCAAACCCA CTCTCTCTGAAAGTGAATTCTATGAGTCTATACCCAACCCAAATCAATAGGTTGAGG TAACAGTTGACCCGATTTCACCTTCAACAAATCATACCTTTCCCGAAGAGAGTGAAC ATGATTCAACACAAGTTCTTTTTGGTTCACCAGATTCAAATGAGCTTGGGGGTAATC CTCCTGTTCCATCAAGACAAGAAGAAAATCCTCCCACTCTCGTAACTCAAGGGTTAA TCCTCCCATTTCTACGGTCACCT
SEQ ID NO:99	Late	LPZ-022	AGGTGACCGTCNCGGGATAGNTGGAGCCNAACAAAGTACNGAANAAANTGAANCG CNCTGGGAAGCGNGCNGAAANNTGGNCANACNTGCCCTNCNACTCGGTTACCCAG CCNTTCTCTACCNANAATTATNACNNNANAGCNCCATGCTGGGTTTGTNANAAAAN AACNGCTNTTGATAAAATTACATAGANTNNNGAACACGTTAAGAGGAATATGGTTCC ANATNCATTNTNAATNANNANTTAAAAACTNNNTATGTNCTAGNGTCNCCT
SEQ ID NO:100	Late	LPZ-023	AGGTGACCGTACAGCACAGGTATACAAATCATAGAAATGGGCTTCTGTCCAACTGT CAGCAGAAGCGATATGAAACCCAGAAGCATCAACTCTGCTTTCAATTTTTCAAGCG CTTCATATAGAGCCTTTTTATTTCTTCTGGAGAGCCAATTGCTAGCATAATGAATAC CATGTTCAAGAAGTAAAGAGATGACCACAAATGCCAAACAAACAACTGCTACTGCC CAAGTTAGGAGTTTGCTCTAGAGAACGGTCATTGCCACGGTCACCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:101	M,L	LPZ-024	AGGTGACCGTGGATATGGGAGCAGAGCCGTCCGCAGTGGATGCTGCAATTCAACT TGAAGTGGCAGAAGCTGTGAAGACTCTCCAAATGGACAAGGCACGAAGACAAAAC CAAGACAAGGATGAGGGCAAGAGTGGCAACGCTGATTCAGATGACTTGAATGAAAT GGAAGTCAAAGCTAAAGCAGCCGAACAACTGCTTGCTGTGCATGGGGCAGCATTA CTACAGAATGCTCTGAAAGAAAATTTGTCGAGTCATGAAATGCGGGTTGGTTCAAA TACAAGGGAGGAAGGTGAAGTTAGAAAGAACAGAAAGGGCATCAACGCAGACCCC TCACTGATATCGGCAACACTACGGTCACCTAAGCCAATTCTGCAAATTTCCATCACT GGCGGGGCCCGCTCCAACTTCCTCTAAAAGGCCAATTCCCCTATATGATTCTTATT ACAATCCCTGGCCCTCCTTTTCCACTTCT
SEQ ID NO:102	M,L	LPZ-025	AGGTGACCGTAGCAGGAGAGAGGAGATCCACAACCATGGTTTTCGTCAAAGCCCA GAAAACCAGGGCCTACTTCAAGAGGTTTCAGGTCAAATTCAAGCGCAGGAGAGAG GGGAAGACCGATTACAGGGCAAGGATCCGCCTGATTAACCAAGATAAGAACAAGTA CAACACACCCTTGCCAAAAAAAAAAAAAAAA
SEQ ID NO:103	Middle	LPZ-026	AGGTGACCGTATGAGCAAGGAGGGAACAGTATGACAGGCAGTCAAAGCCCACGAG GGGTGCCCCACTGCCTGCAGCAGCGCACTTACTTGGACTAACAAACTTGTATCGTG ATTAAAACGATGAACATCGTATTGTGGAGTGGAGCCACTCGTGACCTGATTCTGTC CTAAGTACTTGGTCCTGGAATACAATATTGCACGGTCACCT
SEQ ID NO:104	All	LPZ-028	AGGTGACCGTCAAAGTACAATGGAGTCATATATCCACTTGAATTGAAACCTCTAATT TAAAAGTTCTCAAAAAATATTTTATTTACAAAACAGGGAAAATAAAAAATGACTCTAT CAACTATACAATCCTAACATCCATCTCCCGACAGACCTCCAGTATATGTACAAGGC GCTGAAAGAAGGCTGATTATTTTCTATTCCAGCTCGCATAACGTGGTTCTTCTGAG GCTTTGCCTATTCCTTTCTTTAAAATCTTTCGCACGAAAGATTGGCATTGACCTTCG GCTAAATCTCAGACTCCAGGGAACCTTGGACTCCCTTTAAAACCTAGAGCTACTTTT TACGAACCCCTGCTTCTCTTGAACACTTAGGGAACTTATACTTACAAAACTTCGGGA ACTCCACCCCCTAGCTTTGCAGGACTCCAGCAGATTCCCCAAACTGCCAGAAGGCA TATTTCCATGCACTGTTAGGGGTGAATTCCTACTATCAAAACCCCCAAAACATCATA
SEQ ID NO:105	Late	LPZ-029	AGGTGACCGTATGGGAACAAGTATGGGAACAAGAACGTTATTACATAAAAGATGGA GATGCAACACAGCATAAATTGATGCTAAGTTTGTTACAATGATGCATACAGCTTAAC CAAGCTTGGAAATGACATCATTAAGTGCGGTCACAGCCTCTGCATAGTATTTCTCT GCCTTGGGTGTATCCTTGCTCCTTGCAGCGTAGTCCAGGTTGTCAAGGGTTGTCAA AAAGCTTGGTGGTGAAGGTTTTGAGGGGCTTCTTCTGGTCCTTGGGCTTTGAGGA GATAACGGTGTTTGAAGTCCTTAGCGAAAGTAAGAAACCTTTGGAACCGAAGTCCG TTCTTGACGTTACCGCACGCCTTCCTTATCTATCACTTTTTCACCTCCAGAAATTGC TTCCCGAATCCCTTGCTCTCCCACCCCCTGTTCCCCC
SEQ ID NO:106	Late	LPZ-030	AGGTGACCGTAGTGTTGCCGATATCAGTGAGGGGTCTGCGTTGATGCCCTTTCTG TTCTTCTACTTCACCCTCCTCTCTTGTATTTGAACCAACCCGCATTTCATGACTCGA CAAATTTTCTTTCAGAGCATTCTGTAGTAATGCTGCCCCATGCACAGCAAGCAGTTG TTCGGCTGCTTTAGCTTTGACTTCCATTTCATTCAAGTCATCTGAATCAGCGTTGCC ACTCTTGCCCTCATCCTTGTCTTGGTTTTGTCTTCCGTGCCTTGTCCATTTGGAGAG TCTTCACAGCTTCTGCCACTTCAATTTGAATTGCAGCATCCACTTGCGGAACGGTCT GCTCCCCATATCACGGCACCTT
SEQ ID NO:107	Late	LPZ-031	AGGTGACCGTAGTGTTGCCGATATCAGTGAGGGGTCTGCGTTGATGCCCTTTCTG TTCTTCTACTTCACCCTCCTCTCTTGTATTTGAACCAACCCGCATTTCATGACTCGA CAAATTTTCTTTCAGAGCATTCTGTAGTAATGCTGCCCCATGCACAGCAAGCAGTTG TTCGGCTGCTTTAGCTTTGACTTCCATTTCATTCAAGTCATCTGAATCAGTGTTGCC ACTCTTGCCCTCATCCTTGTCTTGGTTTTGTCTTCGTGCCTTGTCCATTTGGAGAGT CTTCACAGCTTCTGCCACTTCAATTTGAATTGCAGCATCCACTGCGGACGGCTCTG CTCCCATATCCACGGTCACCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:108	Late	LPZ-032	AGGTGACCGTCGTGAAATAGCGAGAACGGCGTGGAACATCGCAACGGCGGGGAG GCTGGCGGACGTTGCACGTTTCTGGAAGGTATGCGGCTCTCTCCTCCGCCTCAGT TTCCATGAAGAGGTCCTCCCTGGTTGAATCATACGATTGCGATTGATCGAGTACTT GCTGTATGGCTCGGCATCGGCATTGTGGAGACATTCTTTCCTATTCCTCGCAGCAT CTCTCCGATGGTTGCTCTCTCCGGAGCTCCATGTTATCCCCGGCACTGAGACAGTC GCTGCCGAATCGCAAGAGCTTCTTTGTTTTTTGCAGGCTTCTCCAAACATAATGCCT CCGGGCCCCTCAACCGAATTCTGCCAAATCCACCCC
SEQ ID NO:109	E,L	LPZ-033	AGGTGACCGTGGACGACAGTGAGTGCAGTCATCATGCTCTCCAGTGGACTTTAAG CAATCTGCATCTTTATGGAAGTGATGTATCTCTTGTGGTTTTTCATGCTCAACCATT GGCAGTCTTCAACAGTGCTGCAACAATGGGCATAACGTCTCCCGAATTAATTGAAA CTATTGTGAATCAACAGATAGGTTTCTGGTCACATCTAGCAATACAAACACAAATAA CTGTGGAACAGAGCCACAAAACTATGCTTCAGAGCATCTAATTACACATATCTTCTC TAAAACCCTTGCATAAAAAATAAACTGAATCTCGACCTTAGCACTATTGCCACCATC ATCTCAAGCAAACATTCTCTAGAATACCATCTTCACAATGCACTAAAGTTACATAAG CACTGAACTTAAAACATTTCTGTGACGAATGAAGGACCAATTCATCATACTCAGCCT TTGCATCCAATCTGTTGAATGTGCTGAAAAATGCCCAATAAACCTCCATCCAACACT GTCTTCCTCTCTGAGGTGCACACTGATTTCTGCTGCTGAACCAGTCGGGATTCCCT GCTCAACGTCCC
SEQ ID NO:110	Middle	LPZ-034	AGGTGCCCGTGGAACTACTGTTAAATCTGGAATCCCTTGTCTAGCTGTAAAAACTC GACAAGTGCATGTTGGTATTAGTAGGGTTAACAGAAGGGTTCTTACCCAGATTTAC CCCTTTGGCGGAGATATTTAAAAAAAAAGAATTGTCATTATGGTAAATAGGTGTGAC AGGTTATCAATAGAATAACTGACGAGAGTAAACTGATAATTATTAAGGTTAAAGTGT TCGTAAAGGAGACTTGGACTCTAGGTTGGATGCCTACACTTAGAGCCGTTCCCGCA CTTGGACGGTCACCT
SEQ ID NO:111	Middle	LPZ-035	AGGTGACCGTCCAGTGCGGGAACGGCTCTAAGTGTAGGCATCCACCTAGAGTCCA AGTCTCCTTTACGAACACTTTAACCTTAATAATTATCAGTTTACTCTCGTCAGTTATT CTATTGATAACCTGTCACACCTATTTACCATAATGACAATTCTTTTTTTTTAAATATCT CCGCCAAAGGGGTAAATCTGGGTAAGAACCCTTCTGTTAACCCTACTAATACCAAC ATGCACTTGTCGAGTTTTTACAGCTAGACAAGGGATTCCAGATTTAACAGTAGTTCC ACGGTCACCT
SEQ ID NO:112	Late	LPZ-037	AGGTGACCGTATGGGAACAAGAACGTTATTACATAAAAGATGGAGATGCAACACAG CATAAATTGATGCTAAGTTTGTTACAATGATGCATACAGCTTAACCAAGCTTGGAAA TGACATCATTAAGTGCGGTCACAGCCTCTGCATAGTATTTCTCTGCCTTGGGTGTA TCCTTGCTCCTTGCAGCGTAGTCCAAGTTGTCAAGGGTGTCAAAAAACTTGGTGGT GAAGGTTTTGAAGGGCTTCTTCTGGTCCTTGGGCTTTGAAGAAATAACGGTGTTGA AGTCCTTACCAAAGGTTAATAAACCTTTGGAGCCGAAGTCGTTCTGGACGTACGGC CACCCCTTCCTTATCTATCAGCTTTTTCACCTCCAAGAATTTGCTTCCCCGAATTCC TTTGCTCTCCCAGCCGCCTGGTCCCCCGAAAAGGGCTGAATATAAAACCGTCCTCA ACGGCATTCCATTCCTCCCTCGTCTGAAACACTTCCCCGCTGCCCCCGAGGTGAA GGGCCATCAACTTGATGAACGGCTTTTGCAAGGCTCTGACCCCGGCCCCGTCACT AACCAATTCTGCAATC
SEQ ID NO:113	Middle	LPZ-038	AGGTGACCGTGGGGAACAACTACATGACAAATCATTTCTTTGTGGTGGATGTACTG GACACCAAATAAGTGTTGAGAGTCCACTGGCTCTGTACGCGTGGCAGAATCACAAC GGACTTGAGAAAGTTGAAGATGGAATTTGTATCGCTAGATGGCCAGACCATGTTGC TTCAAGGGATGCACTCGTAACCCCCACAGTCTGTCTCTACCCACTAGATGGAGGCT GACATGAGACATGGAGACATTAATTGGGTTGTGGAGTTAAAGATCTCTCACGTTCG GGGAAAATCCAAGCCATCATACTTATATATCCGTCCCGTGCATGTAACCTCCTCCA CTCTGTCCCTTAGGCCCGTTGTTGCCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:114	E,L	LPZ-039	AGGTGACCGTATGAGCAAGGAAANNACCGCACTGGCTCCCAGCAGCATGAACANC CAGGTCCCAACCATANACCNCNTGGAGAANGTGATCAAGATATTAGCGACAGTGTN ATTGTACNTCTCNCCAAACACATTATACACGATAAGAGAGCNTAAACTACTCTATTC CTTTGACGNAGTGACTACNTGAGTANAAGCGATCATTATCTTGCNAACTTTGCATGA AAAACAACAAACCCACNTCCAGTTTCTCTATANTCTGGCCCCACNATGAATAANANT CCTGCCATAATAATGANTCTTTGTCCCCANAGANAAATTNNATAAGACAGGAGCCC ACTGTTGCTTGCATGACTACCANTCACTTTAAGGCGTTGCGAATCCCGGTCCTAAC CATCTCCATACCATNGGCANNCTTTACTTTCCAACTGCCCAAGACTGTGAACAGGG CGGTTCNNACCCTATAANTTTTAGCCTCTNNTCGAANCNCTTNTTTTCGTTCCCCGG AAANCCGNTTCCCACCCTTTGGAACCTTTTTTTTTTGCCGGGCCCCAGGCNAATTC TNCAATTCCCCNCTGGGGGG
SEQ ID NO:115	Late	LPZ-040	AGGTGACCGTGGCGGAGGTTAGGGAAGTTTGACTTCTCATTTTCTCACGCACTCCT CTCCCTCGTAACCTCGGTCGAGTCGATGGCGGCTTTTTAGTCGAGTGTGCTAACG CACCCTCCGGGCCTCAAAATTTCCAGCTACTCGTATTTGATCAATGCTGAAATCGC GTAATCACGTAGATAATAAAGCGTAATGAATTCTATAATGAAGCATGTTTCTCTATA GTTCATGTTGCCGAGAAGGAATAATGAAAATGAAGCCTTATATATTATCTGGGGCTC AAGGAGATGTTATCTTTTCTCTTCCTTGGTTAGAGACCGTCACCTTCACTTTGAATT GGATAAAGCTTCATTTGTTTAAGACCTCCCACCCGTAAATACATACGGTAGCCTTCT TATGTTAGAAACATACGTCACCTACGCAGAATTGTTAGAATGAAATGA
SEQ ID NO:116	Late	LPZ-041	AGGTGACCGTGGAACAAGATGATTAGTTCTCATGCGGGCCAGGATGATTAGTTCTC CTATGGCAACTGTTGGACAGGATGATTCGTTCTCCTGTGGACAGGATGATTAGTTC TCCTATCGAGGCATCCTACCCAAGCAGTTTGGGACTCATGGGAAGTACCTCTCATC TGATCAATGAGTAGGAAATGGGGTTAGGGACCATTAAGTAGTATTATCGATGGATG CATTGTTGTATCTATTGTACTCCCTATGCTAGAATGAACTCCATTGATCTGGGATCA ATGAATACTGTTTCTGGGAATCATTGAAAATTTGTATGAACACACTCTGAACACTGA ATTTCCGGTTCATTGGAAGAGATGGTTTTAAACACTCTCCTCATCTCATTTCTTCCC CTTCCTTATTCCAACCAAATTTGGGCCACCCTGCCAGGAAATTCATTTGATGGTTGG AAAATACCACGGGCCCTAACCAATTCTGCAA
SEQ ID NO:117	Late	LPZ-042	AGGTGACCGTNCATCTCTACCATNATNCCTCCCTCCCGNCTGTATCANCNGGCNTN NANGTCNTTNNCTANNNNAAGNTTAATCCTATCCCNTTANAGTTGACGGTCTCTAN NCCTAGAAGAGAANCCATAACATCTCCTTGAGCNACACATGGGATATACCGCCANC TTATNTAATACTTTCNCNGCACGGTAACNGACCANAANCATTCTTCACTATAGAATT CATGTCGCTTCATTATCTACCTCATTNCNCCANATCCCCCTTNATCTCATNNATTTAT CTAGAAANTTCTGAAGNTCCNNAAGGGTTCGTTTTGCACCNCCCCAANTAAAAAAN CCCTNCCGNTTACNTCGAACGAAGGTTTTCAAANGAACAGNAATTCCTTTACAAAAA TCAANAATTTTAACTTCCCNAATCCGGCCCCCCNGTNCCCGAAACCCNATTTCTAC GATTGCATCACCCCGGGGGNCCNCTCAANCCNNCTTCTTAAAGGNCCATNCCCNT NNNTGATCCTCTNCCATCCAANGGCNCCTTTCCACTTTTATTGGAAAACCCCCNTT CCCCNTTTTACCCTTNNAAGGCCCCTTCCC
SEQ ID NO:118	Late	LPZ-043	AGGTGACCGTGGAACTACTGTTAAATCTGGAATCCCTTGTCTAGCTGTAAAAACTC GACAAGTGCATGTTGGTATTAGTAGGGTTAACAGAAGGGTTCTTACCCAGATTTAC CCCTTTGGCGGAGATATTTAAAAAAAAAGAATTGTCATTATGGTAAATAGGTGTGAC AGGTTATCAATAGAATAACTGACGAGAGTAAACTGATAATTATTAAGGTTAAAGTGT TCGTAAAGGANACTTGGACTCTAGGTTGGATGCCTACACTTAGAGCCCGTTCCCGC ACTTGGACGGTCACCT

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:119	Late	LPZ-045	AGGTGACCGTGGGGGATGGGGCCGTGGGGAAGACTTGTATGCTCATCTCCTACAC AAGCAACACGTTTCCAACGGATTACGTGCCGACTGTTTTTGACAATTTTAGTGCAAA TGTGGTTGTTGATGGCAATACAGTAAACCTTGGCTTGTGGGACACTGCAGGGCAA GAAGATTACAACAGACTGAGGCCATTGAGTTATAGAGGTGCAGATGCTTTTCTGCT TGCCTTTTCTCTGATCAGCAAGGCTAGTTATGAAAATATATCAAAGAAGTGGATTCC AGAACTTAGACATTATGCACCAAATGTGCCAATCATTCTTGTGGGAACTAAATTAGA TTTGCGTGATGACAAGCAGTTCTTTGCTGATCATCCTGGAGCAGCCCCTATAACAA CAGCTCAAGGTGAAGAGTTGAAGAAGCAGATTGGAGCAGCAGCATATATTGAGTG CAGTTCCAAAACCCAGCAGAATGTCAAGGCTGTTTTTGATGCTGCAATTAAAGTGG TTCTTCAGCCACCAAAGCAGAAAAAGCGGAGAAAAAAGCAGAAAAATTGTTCTATTC TCTAAGAAAAATGTGGATGTTCTGAACGCNCTTCACTGACAATAANGNTGACGTNG GAATATCTTCCTCC
SEQ ID NO:120	Late	LPZ-047	AGGTGACCGTAAGCACAAGTCGTCAAAATTATCTCTATTCCGGCAGTAAAAACCTAT AGCTAATGATGGATCAATACCACTAAGTGGCAGCTGGCGTACATCTCTGCAATGAT AAGAACCAGTATCAGTCCCCATATAATCAGGAGATATCTCCAGCACCTGCTGCACT ACATGTGGATCTTAGTACAGAGCCTGATCATCCTGAACACCAACAATATACGTTGAA GCTCCGGGCTTTCCACCAGCAATACCAAGACTTTGGGGAAATGTGAACGTTTCACG AAGTGATGGTACATACCTTGGGTTGATCTTCTCTACACCAAGAACAAGCGGCACCA AAATCAGGATAGGCACTTGGTCTTCCCCTTCTCCATTGGACCACTCTGAACACAAG CCTCGCAGCATCATCAATGCAGATAACTGGGCGCCCTCCACGGTCACTT
SEQ ID NO:121	Late	LPZ-049	AGGTGACCGTGCCATAGCGCATGGCGTGTAACTGGATGAGACCGCATGGCTCAAA TCTGCTAGGAATCAACATGAAATCAGCTCCAGCTGTTATCATATGAGCAAGTGGCA CGTTAAACTTTGCTACTCCCCTGACGTTGTCTGGATATTTCTCTTCAAGCTCTTCAA GCTGCTTCTCCAAGTACTTTTTACCGGTGCCTAGGATAATTAACTGCACGTTTTCAT CTGCAATTAGAGGGACAGCTTCAGCAAGAATATCTGGACCTTTCTGCTCTTCAAGT CTTCCAATAAATCCTATAACAGGAATATCTGGATCCACGGTCACCT
SEQ ID NO:122	Early	LPZ-051	ATGTGACCGTCAAAAGGGCATATAAATCGGGGAGCTCAATGGCAAGAATGTACGAT TTCTGGCCTCAAGTCGCCCTGAATTTGGTCAACAACATCTTGATAGAGCGAGAGGA CGCTCCCAATTAAGATCTGGAAACTGTCGAGAGTGATTGAGGTCATTTTTAATCTAA ACTGAATTGTGGGGACAATTTTTCAATTCAGATCCTTCTAGCAAAGCAAAGCAAAGC TTAACAGTATTGTATCCATGAGAATGGATTCTGCACAGGTCAGGCTCCACGGTCAC CT
SEQ ID NO:123	All	LPZ-053	AGGTGACCGTGGAGAAGAGAACGCTTTGCCGACTCTCTGGGATGCCCTTCCCTCC ATAGCCGTCGTGGGAGGACAGAGCTCCGGGAAATCCTCTGTGCTGGAGAGCATCG TTGGAAGGGATTTTTTACCGCGTGGATCAGGTATTGTTACTAGACGGCCGCTTGTC CTTCAACTTCACAAGACTGATGAAGGCAGCAGGGATTACGCCGAATTCCTTCACCA ACCCAGAAAGAAATACACCGACTTTGCACTGGTAAGGAAGGAAATTGCGGATGAGA CTGATCGAATTACAGGGCGTTCCAAGCAAGTCTCAAGTGTCCCAATTCACCTTAGT ATTTATTCACCCAATGTTTGTAAATTTGACTCTAATTGATCTCCCTGGGTTGACAAAA GTGGCTATTGACGGTCACCT
SEQ ID NO:124	Middle	LPZ-054	AGGTGACCGTGCAATATTGTATTCCAGGACCAAGTACTTAGGACAGAATCAGGTTA CGAGTGGCTCCACTCCACAATACGATGTTCATCGTTTTGATCACAATACAGGTTTGT TAGTCCAAGTAGGTGCGCTGCTGCAGACAGTGGGGCAGCCCTCGTGGGCTTGGA CTGCCTGTCATACTGTTCTCTCCTTGCTTCAGGCTCTACTGCTGTTGCTGCTGCTG ATACGGTCACCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:125	Middle	LPZ-055	AGGTGACCGTACATACAAGGTCTTATCACCAGCAGCAAGAATAATCAGTTGGCCAT CTTCTGCAGGCTTCTTGCTGCCTGAGACAGGAGCCTCAAGAAATCTTCCCCCCTTT TCAATGATTGCCTCATTGATCTTTGTTGAAGTGATAGTATCAACTGTTGACATGTCA ATGTATCCTTTTCCTGTACACATTTGCTCTAGGACACCATCCGAGAGGGCAGCAGG AGGATCAGACAGGATGGCTATGGTATAGTTGCACTTCTTTACAACTTCGGCAGGAG TGCTTCCTATGGAAGCACCTTGCTGAACAAGTTCTTCACACCTAGACATTGTCCTAT TCCACACGGTCACCT
SEQ ID NO:126	Late	LPZ-056	GGTGACCGTACATACAAGGTCTTATCACCAGCAGCAAGAATAATCAGTTGGCCATC TTCTGCAGGCTTCTGGCTGCCTGAGACAGGAGCCTCATGAAATCTTCCCCCCTTTT CAATGATTGCCTCATTGATCTTTGTTGAAATGATAATATCAACTGTTGACATGTCAAT GTATCCTTTGTCCTGTACACATTTGCTCTAGGACACCATCCGAGAGGGCAGCAGGA GGATCAGACAGGATGGCTATGGTATAGTCGCACTTCTTTACAACTTCGGCAGGAGT GCTTCCTATGGAAGCACCTTGCTGAACAAAGTTCTTCACACCTAGACATTTGTCCTA TTCCGCACGGTCACCT
SEQ ID NO:127	Late	LPZ-057	AGGTGACCGTGGAGGGGCTCCAGTTATCTGCATTGATGATGCTGCGAGGCTGTGT TCAGAGTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGC CGCTTGTTCTTGGTGTAGAGAAGATCAACCCAAGGTATGTACCATCACTTCGTGAA ACGTTCACATTTCCCCAAAGTCTTGGTATTGCTGGTGGAAAGCCTGGAGCTTCAAC GTATATTGTTGGTGTTCAGGATGATCAGGCTCTGTACTTAGATCCACATGTAGTGC AGCAGGTGGTGGAGATATCTCCTGATAATATGGGGGTTGATACTGGTTCTTATCAT TGCAGTGATGTTCGCCACTGCCACTTAATGCTATTGATCCATCATTAGCTATAGGTT TTTACTGCCCGGAATAGAAATAATTTTGACAACTTGTGCTTACGGCACCT
SEQ ID NO:128	Late	LPZ-058	AGGTGACCGTGGAGGGGCTCCAGTTATCTGCATTGATGATGCTGCGAGGCTGTGT TCAGAGTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGC CGCTTGTTCTTGGTGTAGAGAAGATCAACCCAAGGTATGTACCATCACTTCGTGAA ACGTTCACATTTCCCCAAAGTCTTGGTATTGCTGGTGGAAAGCCTGGAGCTTCAAC GTATATTGTTGGTGTTCAGGATGATCAGGCTCTGTACTTAGATCCACATGTAGTGC AGCAGGTGGTGGAGATATCTCCTGATAATATGGGGGTTGATACTGGTTCTTATCAT TGCAGTGATGTACCCACTGCCACTTAGTGCTATTGATCCATCATTAGCTATAGGTTT TACTGCCGGAATAGAAAAATTTTGACAACTTGTGCTTACGGTCCCT
SEQ ID NO:129	Late	LPZ-059	AGGTGACCGTGCTAGGACACACAATTTCTCAGCAAGGATTACAGGTGGATCCTAAC AAAATTGCTATAATTCAAAAGGTTCCACCTCCTTAAAAGGTAAGAGATGTTTGGAGT TTTCTAGGCTTGGCAGGATATTATAGAAGATTCATCAAAGATTTCATTAAGCTAGCC TCGCCATTGTCTAGCCTCTTAGGGAAAGATGTTGAGTTTCAATGGACTGATGACTG CCAAGGGGCTCTGGATGAGTTGAGAGATAAGCTGGTATCCGCCCCGATCTTGAGA GGTCTAAACTGGGCCCTACCTTTCCACATCCACATTGATGCCTCGAACAAAGCCAT AGGGGCAGCCTTAGGACAAGTTGAAGAGAAAATACCATATGCCATATACTTTGTCA GCAAAAATCTGTCTAAGGCAGAACTGAACTATACGGTCACT
SEQ ID NO:130	Late	LPZ-060	AGGTGACCGTCATATTCCCCTCTATAGCAGCACTAACAATCCATTTTCTGAGTGCAT CAGAAAATCAACACACGGTAAATGTCTTGAGACTAACGAGAAATTAATAATCACGTT GTACAAAGAACAGTATGTCCCGTCACGTCACGAGTGCCCTGAGAGATCATCCAACT TTCTCTGAACCCTCGTGTTACACGCACGCAAAATCAAGGATCAGTTGTAGTTATTGC TGGCGTGACAGACGTGACACCTACTGTTCCGCTACAAACGATATAATTGAATCCAT GATCGGATTATGTATTATGATCTTAGCGCAGTGGTTATGAAATTATGATGAATTTGC TTATGATTTTCTCAGCGTTTGTGGAAGAATCTCGCTATTGAAAACTTCCCCGTATAT TTCCAAACTTATTATCATCCCACGGTCCCT

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:131	Late	LPZ-061	AGGTGACCGTACAGCATTTATTGATGTTCTATTTTGTTGTTTGCAAGTTTTTCCGATT CGCTGTGAGGCACGGAAAACGAGATAAGTTGTAAAAGTTTGCTCGCTGATTTGAGG CACGGAAAACGAGATAAGTTGTAAAATTTTGCTCGCTGATTTTTTGCTGAATATTTC TCTCACTATAAAAAGCATTTTCCAGAAATAAGAAGGAGCTTTCGAACTGGTTTTCCC CAAGAGTTGTAGGGGGTTTTTCCACGGTCACCT
SEQ ID NO:132	Late	LPZ-062	AGGTGACCGTATTTATGGTCGCAGGCACAAATTCTGCTACTGTAGAAGGGTTCTTA CCAACTTTAGGTAGAAGGCGAGGAGGGCTTTATTAGTACAGTTCTGTGTAATCTTA ATGATATTTTTTGCACTATTATTTTATGGTAAAAGGATTGATTTGTCTTTTGCAAAGG CCTTAGGATTGTTTATTTACCTTTGGGCTAAGGGAGGAGGTAAATTTTTCACATTGG GAAAAAAAATGCCTCGGTCGTTGTCACGGTCACCT
SEQ ID NO:133	Late	LPZ-063	AGGTGACCGTGCCAGTATGACAGATGGAACCATGCAGCTAGCCACCAAATTGTAAA CATCAAATTTTGTCTTCAATATAAGTTGCAAATTCTTAATTAATTATGATCACCATTTC AACGGTCACCT
SEQ ID NO:134	Middle	LPZ-065	AGGTGACCGTGAATAGAAGCGAACACATCCTTGTTGCTGAATCTAACGACCAATCG GTATTTGGGTGTGTTGTACTTGTTCTTATCTTGGTTAATCAGGCGGATCCTTGCCCT GTAATCGGTCTTCCCCTCTCTCCTGCGCTTGAATTTGACCTGAAACCTCTTGAAGTA GGCCCTGGTTTTCTGGGCTTTGACGAAAACCATGGTTGTGGATCTCCTCTCTCCTG CTACGGTCACCT
SEQ ID NO:135	Middle	LPZ-066	AGGTGACCGTGGTAGAGGAGGCAGGCACTCATCTAACAGTCGAAAGCCCTTTACA AAGGGGAATGGTACCAGCATAGAGAAGAAACACAGACGGTTTGAAGAGGATGATG GATCTGCCATAGATGAACGATCAAATAAGGTTCAAAAGCTGGAAAATGATGGTGAA TTCCATGCATCCCACTTGGCTCTGTCCCTCAAGTTGAATATACCTGGACGAGAGGT ATTGCATTTCCCAACGGTCACCT
SEQ ID NO:136	Middle	LPZ-067	AGGTGACCGTACTGATAATAGAAGAGGCAGGGAAAGAGAAATCAATGATAATAGAA GAGGCAGGGAAAGGGAGATCAATGGCATCATGCTACTTCTTGTAGCTGTTTAACCT TAGTGATGTAATCTTCCATGGCAGACTCGGGGGTTTTATCTTTAAGTTGAATTTCCA TGCATCCCCTTGGGCTCTGTCCTCCAGTTGAATATCCTGGAACAAGAGGTTTTGCT TTCCACGGTCCCCT
SEQ ID NO:137	Late	LPZ-069	AGGTGACCGTGAGAAGGCAACTTTATCCCCTGCTAAACCAAGTCCAGAAATGAGGA AAATATGTGAAAACTGAATTGCTATATATGATGCCTAGTCTTGGCCTCTCAATTACA AGTTCAACGTCTTCAAATGATTGAAATATGGACCTTCTTAACCGTTCTGGAAATCTA TCAATCTTCAAAATTTTGAAACTTTGCCTCGATCTTGGAGTGATCAGACTTGATTTCT AATCCTAGAAATACCCTATCACTGGCTACCTGGTCTGTACGGTCACCT
SEQ ID NO:138	Late	LPZ-070	GGTGACCGTGGGATAGGCAGAAGCAAGAAACACAGAAGTTCTTCCGGGAATGTAA GCGCTGACAGTGGGGGAGAAAGTAGTGAACAAGGACATGGTCGGTATGAAATACA TGGCAGGCGATGGATTTCAAGGGATTAAGCATCTCAATGGATATTTACTATTGGAC TGTAGTAACTTTCGCCATCGCTTTTTGAACACATCTGTGGCTTAACTGTCATCTGTA ATGGTAAGCGAACCAGGTTTTGTTCTGAACCACTTGTATGTACGGTCACCT
SEQ ID NO:139	Late	LPZ-071	AGGTGACCGTGGTGGAGCGATTAGTGATTGTGATAAAGGGAGCATCAATATCTATG TAGACGCCGTATAAAGGTGGAAAAGGTATGTTTTGCAGGTATTTCTTTGTAAATGGT TTATAATGGGTTAAGCTCGGATATATGAGGTTTATATATAAGTCCTGTTAGTGTCAG TCTTACCAGCCTTCCTCCAGTGATCAAATGTGCTCTAACAAAGTGATTTTGAAGTGT CAAGGTCAAATTATGTCATTTCAGTGAGTCTTCAAACAAAATTTGGTCACTAGGCAT TAGGTCTAAGGGTTTGCTTGAACTCCCTCTAGAGTTGTCCAAATGGGCGGGCTATG TCATCATTTAAGCTGAATCTATCATCCAATCAATAAGGTTTTTCATTATCATGTCAGT GTCTAAATGAGTCATTTTACCGTCTTGTTCACGGCTTCACTTGTGCCTTTGGCAAAT TCAATTCCCTCCTCCAAGGGTTTGAAACCAATTCTCTTGGACGGCCCCTAAACCAA ATCTGCAAAATCCAC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:140	Late	LPZ-072	AGGTGACCGTGGTGGAGCGATTAGTGATTGTGATAAAGGGAGCATCAATATCTATG TAGACGCCGTATAAAGGTGGAAAAGGTATGTTTTGCAGGTATTTCTTTGTAAATGGT TTATAATGGGTTAAGCTCGGATATATGAGGTTTATATATAAGTCCTGTTAGTGTCAG TCTTTCCAGCCTTCCTCCAGTGATCAAATGTGCTCTTACAAAGTGATTTTGAAGTGT CAAGGTCAAATTTTGTCATTTCAGTGAGTCTTCAAGCAAAATTTGGTCACTAGGCAT TAGGTCTAAGGTTTGCTTTAACTCCTTCTAAAAGTTGTCCAAATGGCGGGCTATGTC ATCATTTAGCTGAGTCTATCATCATCATAGGTTTTCATTATCATGTCAGTGTCTAATG AGTCATTTACGTCTTGTTCAGCTCAGTGTGCCTGGCAATTCATTCCTCTCTAAGGTT TGAACCATTCTCTTGACGGCACTAAGCCAATCCACACTGGGGCCGTCTATTGAATC AACCCGGACACTGGGTTACAGGCAAC
SEQ ID NO:141	Late	LPZ-073	AGGTGACCGTCCAAGAAGAAATTGGCTTCAAAACCCTAGGAGAGGGAAATGAACTT GCCAAGGCACAACTGAAGCATGAACAAGACGTAAAATGACTCATTAGACACTGACA TGATAATGAAAAACCTATGAATGATGATAGACTCAGCTAAATGATGACATAGCCCGC CATTTGGACAAATTTTAGAAGGAGTTAAAGCAAACCTTAGACTTAATGCTTAGTGAC CAAATTTTGTTTGAAGACTCACTGAAATGACAAAATTTGACCTTGACACTTCAAAATC ACTTTGTAAGAGCACATTTGATCACTGGAGGAAGGCTGGAAAGACTGACACTAACA GGACTTATATATAAACCTCATATATCCGAGCTTAACCCATTATAAACCATTTACAAAG AAATACCTGCAAAACATACCTTTTCCACCTTTATACGGCGTCTACATAGATATTGAT GCTCCCTTTATCACAATCACTAATCGCTCCACCACGGTCACCT
SEQ ID NO:142	Middle	LPZ-074	AGGTGACCGTGATAGACCCCAAGAAAAATAGATCCAACCCTCAGAGGGACAAAGA CTTATAAAGACTAGAAGAGTGAATCAACCTATTCTATTTAGAATATATATTTTTGGGG TGCTTGCTTATCGTTTTGGGGGTTAATGTATGTCGTACTACGGTCTTATGCCCTAAT TTGCCCATTGAAATCAACTAAATTGACAGTAACCGACTAAAAGTTGGTCCACACTAA GATATCGATGACCAACGATCATAAAGGTGTCCATGATCCTAATAGTATATGTGTCAA TTAATGTAACTTTGGTGCTACAACATAAAACCATTCGTGGGGATCCTCCTTTTTATG CGGTCACCT
SEQ ID NO:143	Middle	LPZ-075	AGGTGACCGTGGGACCGACCTTGACTACAGGCCAAAATTTTGACTGTTGACCAGC GTTCACTTCTGTATTTTTGGTTGGTATGAGCAACATTGACTTGCTGGAAATTGACCA GGTTTGACTGGTATTTGGACTTGGATTTTGGCACAGATTTCTAGACAATTTGTATTT GTAAACCTTACAGAAGAATAATTTATCGAAGAAGAAAAATGCTAGGTTTCCCCTCAA GTTTGGGTTTCCCAAGGGAAAAATTGTTGTCCCAATGGTTGAATTTTCCAAAGGTCT CCTAACCCGACAATACCTCCTAAGAATTCCTTAATTTAACCTTTCTTGTTTTCACGGT CACCT
SEQ ID NO:144	Middle	LPZ-076	AGGTGACCGTGAAGGAGCAGCAACAATTTGATTTTGTTTGGGTAGATCGGGGATTT TCTCGTGGAACATACCTGATTGAGTATAAACTAAGTCAAGGTACTGTGCTTGAGAAA TTACTTGCTCCTCAGTAACTACTCTGGCCTTAGCTACATCCTCAGTGATCTTGGGTA GTAAAGATTTTACAAACCATTCAGCTAAGATCTGATCCGGGATATAAACTTTCACTA AACGTCGTCGACGTCTCCATTCATGGATATGATCTGAAATGTAAGTGGACGTTGAC TGCTTTAACGAAGTTAATAATTCTGTGCCATTTTCATATCTGACGGTCACCT
SEQ ID NO:145	Late	LPZ-077	AGGTGACCGTACCTAATGGGAAGACACTTCAAGGTAAAAACAAATCATGATAGTCT TAAATACCTTTTAGAACAAAGATTATATTCAGAACAACTTGCTGGAAGTGTACCAAG TATGACTGGTATTGAGACTTAGATCTTCGCACAGATTTCAAGACAATTTGTTGTTGT AAGACTCACTCACGAAAAGTGATGTGGATATGAAGAACTTCCCTGTCGCCTCTTGG TTAGGAGTCTCCCACTCATAGGAATTGTGTAACTTATAACTTGGTCCACTAAAGAAG TTAGGTACAGTGTGTTCCTTTACCAGGTTCCCTGTTGTAACTTACAAATCTACGGCT ACCT
SEQ ID NO:146	Late	LPZ-078	AGGTGACCGTCACTGGAGGTTTGAGATGCTTGATCGGTACTGAAATGAGACATGAT CAGAATAGGACCTTGTTGAGGCCGTGTCTCACCCCCCATCCACAATCTTTTGTAAT TTTGAGTTTCGTTTAGAACATACTTGTAGGATAAAACTTACCTTACTCATGGATCAT GGCTGTATATGTTTATCGACCAGAGACAGATATGCCGAATGAAAGCGAGTCTAGTA TTCTAATGCAATATATTGGTAGTATGGGACATAGTACTGAACACTTGTATAGTACGG TCACCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:147	Late	LPZ-079	AGGTGACCGTGGTCTCAGTTATGCCATATGTCCGCCCCTCCATATGATGCTCCGCC TCTATGGGGGTCTTTGCGATGTTGATATCTAGTAGTACTTCTTGTCCTATTGCAGCA ACCTGTACTGGTGTTGGTGTTGGTTATGGGTCTCCTACGCGATGGAGATATGAGAC ACCCATAGGTCGAACAGGTCTAATATCTGGAATCCAACGCTATTTGTTGTAGAAGAA ACGTTGCTCCCGTCCTTTAGCTTTGGCTGGTCACTATCCTTACGCTCCACGTACGG TCACCT
SEQ ID NO:148	Middle	LPZ-080	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCATTGAT CTCCCTTTCCCTGCCTCTTCTATTATCAGTACGGTCACCT
SEQ ID NO:149	Late	LPZ-081	AGGTGACCGTCAAGGCAAAGTGTCATGCCACTCATTGGAATTAGTTAATATAGCTA ATTTGAGATATTACAGTCAACTGTGGGTATATGTATGTGAGATCAAGGTGCAGTTTA GATATTATCAGTGGTGCAGTTTAGATATTATCAGTGTTTGTGAATCTGCATACTGCT TTTGGTTGGTTCTAACTACGGTCACCT
SEQ ID NO:150	Middle	LPZ-082	AGGTGACCGTAGACATATATCATGGAAAACCCAAGTAACATACAAACACAAAACACA TGGAAACTTCATAAAACCTCCACTCGTCATAAGCTTTATTGCTATGTTATTGTGGTG TTGCATCGTACTTAGTGGAGGTTATTGTTATGTTATGTGTTCTATTTTCCTCCCGAA CGCCCTTCGGAATTGAGCTAACCGTGGTTAACAACATGTGGGCTTTTTTTCTCGAC AGTATATATATAATAAATCTTTATTTTTTTAAAAACTAATGCTATTGCATTTATATACT GGAAAAAATGATTTTTCTTGTATTATCGAAAATAATAATTTAGTTTCTTGATAATCACT TGGAATTAAGAAATTACAAACCCTAACAACATCAAGAAATTTTAAAACACATAAGCTA GAAATTTTAAAACACATAAGCGTGACAACAAGAAGATCAAATCTAATACTTGCTTGG GCCGGAGATTATGGATTCATGAAGCGATTTGACAGCGTCCATTGATCTTCCTCTCC CACGGTCACCT
SEQ ID NO:151	Late	LPZ-083	GGGGGTAGGGGTGTTTATACTGAGCATACTTCGAAAGTGGTTCACCACCACCATGA TGACTAATTGTTCCTGACTTTGGTAGACCTATAATAAATTCCATAGAAACCTCCGTC CATATTGATGCCGGAATGGGCAACGGTTGTAATGTGCCTGGTACTTTGACGGTCAC CT
SEQ ID NO:152	Middle	LPZ-084	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCTAGACA AATAGCTTTGCTCAACACATCCTGATAGTGTACACTAAATCGCACAACTTTACTACT ACAAAGAAAGATCGTTGACACCTTGACAAATAGCTTTGCTCAACACATCCCAACAAT TTGGATTGCGAATACCGACTCCAATTTGTACTTGATCCATATGTCGTTGCGATGTAC TAGTTCCTCTATACATATGTTTCTGCAAGAATCGGAGTTGGACCTCTTCTTCCCTGT TATCAGCACGGTCACT
SEQ ID NO:153	Early	LPZ-085	AGGTGACCGTGGATAAGAGAACGCTTTGCCGACTCTCTGGGATGCCCTTCCCTCC ATAGCCGTCGTGGGAGGACAGAGCTCCGGGAAATCCTCTGTGCTGGAGAGCATCG TTGGAAGGGATTTTTTACCGCGTGGATCAGGTATTGTTACTAGACGGCCGCTTGTC CTTCAACTTCACAAGACTGATGAAGGCAGCAGGGATTACGCCGAATTCCTTCACCA ACCCAGAAAGACATACACCGACTTTGCACTGGTAAGGAACGAAATTGCGGATGAGA CTGATCGAATTACATGGCGTGCCAAGCANAGTCTCAAGTGTCCCAATTCACCTTAA TATTTATTCACCCAATGTTGTTAATTTGACTCTAATTGATCTCCTGGGTTGACAAAAT TGCTATTGACGGTCACT
SEQ ID NO:154	Middle	LPZ-086	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCATTGAT CTCCCTTTCCCTGCCTCTTCTATTATCATTGATCTCTCTTTCCCTGCCTCTTCTATTA TCAGTACGGTCACCT

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:155	All	LPZ-089	AGGTGACCGTACATACAAGTGCTCAGTACAATGTCATATACTACCAATACATTTGAT TAGAATACGAGACTCGCTTTCATTCGGCATATCTGTCTCTGGATGATAAACATATAA AGCCTTGATCCATGAGTAAGGTAAGTTTGAAGCTACAAGTATTTTCTAAACGAAGTT CAAAATTACATAAGATTGTGGCTGGGGCGTGAGAAACGGCCTCAACAATGTCCTGT TCTGATCATGTATCATTTCAGTACCGATCATGCCTATCATACCCGCCTGGTGACGG TCACCT
SEQ ID NO:156	Middle	LPZ-090	AGGTGACCGTACTGATAATAGAAGAGGCAGGGAAAGGGAGATCAATGGCATCATG CTACTTCTTGTAGCTGTTTAACCTTAGTGATGTAATCTTCCATGGCAGACTCGGGG GTTTTATCTTTAAGTGAATTGCCATGCATCCCACTTGGCTCTGTCCCTCAAGTTGAA TATACCTGGACGAGAGGTATTGCATTTCCCAACGGTCACCT
SEQ ID NO:157	Late	LPZ-091	AGGTGACCGTATAGTGTCAAGCTTTTCTGGATTGGATAATGGACGGCGGCTTGCGA CATACATCTACACATTCTGTAACAAGTACACTCTACTGCAACAGCAGACCCAATTTC ACCTCTTCAGTCAGCCAGAGATCTCGATGGATTTGGGTTGAGGAGGTTGGGGTTCT GCCTGCTTCGGCACGGTCACCT
SEQ ID NO:158	Early	LPZ-092	AGGTGACCGTGCTAAGTAATTATCATCTGTACCTGTGCTTGCTGCAGGAAGTAAAC CAACCCGACTAGTCTTTTTAATAATACAGGGAGCCTTGCCACCAATTTCCTCTTGAA GCACCCATATTGGACGGGTTTGTGTCATCCTCTGTATTATCCTTTTTCATCCCAAGC AGGCTGTCTGTTTTTGTAGTAGAAGGATCACAACACAGATCAGGCCCTCCATAGTA CAAAGAAGAACCGAGGAAAGTATCATTAACGTTCTGACTCCTGCCATGAAGGCTTC CACTATGACCTTGACCCTTTTGTGAATTACTGCCATTTAGACCTTGACTGGCTCTTG CAACCAAATGCCCCAGAATGGAACTTCTTTGTGCTCCAGTTCCATTGTGGTTAGTT GAATCCCTACCACGGTCACT
SEQ ID NO:159	Late	LPZ-093	AGGTGACCGTGCAATATTGTATTCCAGGACCAAGTACTTAGGACAGAATCAGGTCA CGAGTGGCTCCACTCCACAATACGATGTTCATCGTTTTAATCACAATACAAGTTTGT TAGTCCAAGTAAGTGCGCTGCTGCAGACAGTGGGGCACCCCCCGTGGGCTTTGAC TGCCTGTCATACTGTTCCCTCCTTGCTCCTGCTCTTGCTCTCGCTGGGCTGTGGTG AGTTACTAACCTGGTTCGACCCACAAGGGCTTCTCACTAGGGCGTTAGGCTGCATG GATCTGCCAGATATTGTGGTTGCAAGGGACAGAGGCATGAGACACAGGCCTTTGC TTTGCAGAAACTGCATTGCTGACCCCATGTTTTCATCCATCAGTTTTGCTACCTCTC CTTCTGTTATGGACGGTCACCT
SEQ ID NO:160	Late	LPZ-094	AGGTGACCGTATCCGCAGCAGCAACAGCAGTAGAGCCTGAAGCAGGGGACCTAAT TACAGTCAAAAGTCCAGGGCTACCAATGCCTGCTAACAGCGCACTTACTTGGACTA ACAAACTTGTATTGTGATTAAGACGATGAACATCGTATTGTGGAGTGGAAGCCACT CGTGACCTGATTCTGTCATAAGTACTTGGTCCTGGAATACAATATTGCACGGTCAC CT
SEQ ID NO:161	Late	LPZ-095	AGGTGACCGTATCCGCAGCAGCAACAGCAGTAGAGCCTGAAGCAGGGGACCTAAT TACAGTCAAAAGTCCAGGGCTACCAATGCCTGCTAACAGCGCACTTACTTGGAACT AACAAAATTTTTATTGTTAATTAAAAACGAATAACATCGTTTTTGTGGGAGTGGAACC ACTCGTGAACTGAATCCTGTCCTAAGTTCTGGGTCCTGGGAATAACATATTGCACG GGTCACCTT
SEQ ID NO:162	Middle	LPZ-096	AGGTGACCGTTACAGCTAGGGAAGACTTTAAAAGTTTGTAAAACTAAGCATAGCTCT TAAACACTGAAGTTAAAAGACATGATTGGAATGTGCAAGTGGTTCAGTATCCAAATA TTGAAGGTTGCAGAATATGGAGCTACTGTGCAAACGAGTAACTTTATCTATATTTTC ACAAGATCATACAATGGGAAACGTTGAGATAACAACTGCATCGGTGAACCAGAATA GTTATAAAAGTTCTTGCAAGTAAAGGGATGAATAATTGCATGGTTGGAATTAAGAAT GACCATGTAGAGCTGCTATACAGATTCTCCAAGGTTTTATATTTGAGGAGTGCGCG CTATTGATGTTGTGCAAAAATTTCAGAAATTAAGTTCTGCGGCATTTATCAAGGTTG TTTGAGCCATTTAAATAGCAAGTTTTTGTTTCTCCAAGTACTTTCAGGAAAGCAGAT AGCTCTAGTTATAATGCTCCAGTGACAAACACATCTAGTTGGGGCAGTGAATGACG CTTTTGTCATTCTCTTTTGGTTTCAGGCACGGTCACCT

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:163	Early	LPZ-099	AGGTGACCGTGGACAAACTCTAGAACAGGCATAGCTTTCATGTTCAGTTGTTTTTAA AGAGCAGTCCTCGCAGCAGATCGTGCAGCTTCCTGCTTCACTTCCGTTGATTTTCC TGATCTGAAATACCCGTAAACTTGCTGAAGAACCCAAATACTTAATAGCGTCTCTAA ACAAAA
SEQ ID NO:164	Late	LPZ-100	AGGTGACCGTGCCTGAAACCAAAAGAGAATGACAAAAGCGTCATTCACTGCCCCAA CTAATGTGTTTGTCACTGGAGCATTATAACTAGAGCTATCTACAAGCCAAAACAGTG TTTGGGAGAGATTCCATAACGTCATTGCCTCTGCTACACATCATTCATTGGTTCCAA TAATGAAGCCACGTGCTAAGGACATTGAGAGAATCTTATAAAACAAGAAATATAGTA AATTGGGAAATGCATTTTATCGTCTAACCTGCTTTCCTGAAAGTACTTGGAGAAACA AAAACTTGCTATTAAATGGCTCAAACAACCTTGATAAATGCCGCAGAACTTAATTTC TGAAATTTTTGCAAACATCAATAGCGCGCACTCTTCAAATATAAAACCTTGGAGAAG TCTGTATAGCAGCTCACATGGTCATTCTTAATTCACACCATGCAATTATTCATCCCTT TACTTGCAAGAACTTTATAACTATTCTGGTTCACCGATGCAGTTGTTATCTCAACGT TTCCCATTGTATGATCTTTGAAAATATAGATAAAGTTACTCGTTTGCACAGTAGCTC CATATTCTGCAACCTTCAATTTTGGATACTGAACCACTTGCACATTCCAATCATGTC TTTTAACTTCAGTGTTTAAGAGTATGCTTAGTTTTACAAACTTTTAAAGTCTTCCCTA GCTGTAACGGTCAC
SEQ ID NO:165	Middle	LPZ-101	AGGTGACCGTAAAATACCATGAGAAATGCTTTCATCAGGCACCGCTGGTAGGTTTT CTTAAGCTTTTCATTAGGCAAAAGAGGCTCCGTGAGTTGATCGTTAATTCTCTCCTT GAATGCCATATTGACCAGACACTCTGATTAGAAACTGGAATACAACTGCACATATAG TCATTCTATATGATTCATCCTTCTGCACTTCAGCATCCTGCGGCAACTCTTCATCCC GCCATACTGAGAAAAATTATTTGACTCTTGATCATGTGTAGATGAATCTTCATGAAT CTTCTCATCTTCATTCTTGTCTTTATATCTTTAGGAAGTGCATCTGGTAAAAGTATAA ATGCATCTTCACGGGTGCTTCAGTTTTTGCATGCTCCCGGTTCTTCTTGTTTAGCAT GTGGATCTAGCAAATCACTAAATGTAGTTCTCTCAATTGGTCTGGTGGAAATTCTCC TCAATTCGAGAATTACGAATCATCATACCTGAGTAATATATGTTGCCCTGTACATGC ATATGCTGGTTTTTGGCTCCACCATTCTCCAAAGGGCTCAAAAACTATGCGACCCC TGGTTGCCGTAGTGGAAGGTTATACATTGCGTTCCCAGTAGCCACGGTCAC
SEQ ID NO:166	Middle	LPZ-102	AGGTGACCGTGGAGGGGCTCCACTTATATGCATAGATGATGCTGCGAGGCTGTGT TCATCTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGCC GCTTGTTCTGGTGTACAGAATATCAACCCAGGGTATGTACCATCACTTCGTGAGAC GTTCACATTTCCCCACTTCTTGGTGGAGCTGGTGGAAAGCCTGGAACTTCATCAAT CTATCGTTGGTGTGAGGATGATCAGGCTCTGTACTTATATCCACATGTAGTGCAGC AGGTGGTGGAGATGTCTCTGATAAGTTGGGGGTTGATACTGGTTCGTATCATTTGC AGTGATGTTCCCCCGCTGCCCTTAATTGCTATTGATCCATCATTAACTATAGGTTTT TACTCGCCCGGAATAAGACAATCTTTTGACACTTGTTGCTTGGGTCAC
SEQ ID NO:167	Early	LPZ-103	AGGTGACCGTGGCGCCTGACCTGTGCAGAATCCATTCTCATGGATACAATACTGTT AAGTTTGCTTTGCTTTGCTTGAAGGATCTGAATTGAAAAATTGTCCCCACAATTCTG TTTCGTTAAAAATGACCTCAATCACTCTCGACAGTTTCCAGATCTTGATTGGGAGCG TCCTCTCCTCTCTCAAGATGTTGTTGACCAAATTCAGGGCGACTTGTGGCCAGAAA TCGTACATTCTGCCATCTACCTGTTATTGAGCTCCCCGATTTATATGCGCTTTTGAC GGTCAC
SEQ ID NO:168	Middle	LPZ-106	AGGTGACCGTCAATACCATTAAACTGGGGATTCGTCTCAACAAGTCAACATGCTAA CCTCACAGCTCCAATCAAACAACGTCCGTCGAAGGGCGCTCACACTCATCCAAATT ACTTCCCTCTGCAAGACTCACAAAATCAGATTCTTCATGAATTGCTCAAACGAGGCT GTTATGGATGATGCAGCTGATTACTCAAGTGACAGCACTCTGAATCCCCGTCCCAT ATATAGCGACGCGGCGTTTCAGCCGTGACTGGTCGCAACAGCCTCAGTGGGACAA AAGGCCAGAAGCCCCCCAAGGTTCTCACGGTCAG

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:169	E,L	LPZ-107	AGGTGACCGTGTCGATGTTGTTAGATGTGATTAGGGTTTTATTTCTTGATACAGATG CACTGTTTCTCTGTTTATTCTTTTATTTCTTCAATGTATGTTGTCAAATTATACTTAGT CA1GATCTCCTTTTATCGTTCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG TTTAACAATTAAAAGGGGAAATTAGGCCATATCAGCTTGTCGTATGGACCCACATGC ACTGTAGGTCAC
SEQ ID NO:170	Middle	LPZ-108	AGGTGACCGTATGCAGAGTCAAGGTTTAGTTCCTTCAGAGCCTGCCCGAGTAGCA CTGAGGCAGCTCAAGCCATTTCACGTAGGAAGCCCACAACAAAATAGAAATCAGAG TGAGTCTTTGATCGAGTAACCCATAAGTTCTTAGCTCCCGTTCCATCTTAACATAAG CATTTTTCTTCGTCTTCTCGCAGCCGT
SEQ ID NO:171	Late	LPZ-109	ATTGCAGAGGACTTAGAGAGGGAAAACCGTTCCGATCTGGTGAAGCAATTGGATGA AGCGCTCTGGAATTGATTCCCGTTTCTGATGATATCGTACGGCTAAGCTCAGCTCT TCAGGCATTGGCAGACAATACGATTCTTCAAATGAGATGACAGATTTTAAGAAACTT ATAGGATGACATATTTCCTAGCTTGAAGCGGATTCCCCCTACGGTCAC
SEQ ID NO:172	All	LPZ-110	AGGTGACCGTCCGATAAAGGATGAGAATATAGGTAGATCAACCCAAAAACACTCTC AGAAAACGATTAAAGCCTAACCCCAAGATCGTTGAGTAAATTTAACCCGGTAACCTC CACATAAAATATACTTAGCAACAATAAACTCAACAACTAAACTATCCCTTTAAAATTA AATTATCCTTATTTATTTAAAAAAACAAATCCTTTATATACTAAGGTCCCCTGCACAT CTATTACTAAGGTAAAGGAAGGGAATTATATGCTATCATTGTAAACTTTGACTTCCG TATTTATGATCAGACCATGAGTTTGATAATTAATTTTACGCTCTTTACTCCCCATTCA AGGCACGTGCCTGGTGATATATGAACGCCAAATTATT
SEQ ID NO:173	Late	LPZ-111	AGGTGACCGTAGAATACAATCTATGTATCAAAATGCTAACAAAGAGAATTTGTTGTC TAGCTTGTAAATATACAAAAGAAACTCTCACAAGGAGTGAGAAGCACTAAGGCCCT TGGAAAGAATACGTTTCTATTCAGCGGAGTGTATTTTGAGCTACGGCTTGGCACAA CTCATCCTATAAAACAAGACTCTGTGAGAGGGCAGAGACCTTGATCCTGGGCGTG GCAAGCCGGGTGCCTATTGCGGTAAAATCGAGAAGGGGGACCCTGGAAAAGAGAG GCTGAAATTTGTTTCATTCTGCAACTGAAACCTAACCGGAGGCCGAATCTGATCATT TCTAAGACCTTTGGGGTCCTGGGCATCCCATTAAAAGAACGCTGCTAACTCTCCCC TCCACAAAGGGCCAATGCGCTCAGGTCGGGCTTCTCATCTTCACATTTCTTGCCGA AATCTATCTGAATTTGTTGTATTGAATAACACTGCCTCCTACACGGTCAC
SEQ ID NO:174	Late	LPZ-112	AGGTGACCGTGGGCGCCGTGGCTCAAAAGGCCCTCGCAGACGCCCGCTCCATCA AGCTCATGGGCCCCCTCCACCCTCGGGGGGCAAGCCGGGAACGTTGCTGTCAGA CGAGGCGAGGACCTGGAACTGCCGTTGAAGGAACGGTTCTATATTCAGCCCCTCT CGGCGGACCAGGCGCTGCGAGAGCCAAGGAATCCGCGGAAGCAAATCCTGGAGG TGAAAAAGCTGATAGATAAAAGGCGTGGCCGTACGTCCAGAACGACCTCCGCTCC AAGGCTTCTTACCTTCGCTACGACTCAACACCGTTATCTCCTCAAAGCCCAAGGAA CAGAAAAAACCCCTCAAAACCTCACCCCAAAGCTTTTTTGACACCCTTGACAAACCT GGACTACGCTGCAAGGAGCCAAGGATACCCCAAGGGCAGAAAAAATACTTTGCAG AAGCTGGTGAACCGCCCTTAATGATGTTCATTCCAAGCTTGGTTAAGCTGTATTGC ACTCATTGTTAACCACACTTAACGCCAATCCAATCTATGCTGTGTTGCATCTCCACT TCTTAGTTAATAACGTTCTGTGTTCCCAAACTCTGTGCCACACACGGTCAC
SEQ ID NO:175	All	LPZ-114	AGGTGACCGTACAATACAAATAGGTAGTTTATCACATTGTAGCTTATAGAATGTACA ATTGAAATCAAATAAATTCAACCAAACTCAAATAATATGATCATGTGCTCCTCACCTT CTCAGCAAACTCGTAGAGCAGAAAAAAGGATTATGTTAAATCACAGTTCACACATTA GGGTAAATCCCACTAAATGACCTCTCTTCATTATCCAAGTATCTGACACCAACATAT TTCAAACAAATAGTGCAAAAAGGAATGGTGAAGTAAAATAGTCAAAACTAAAAAATA AGCTTAAAATTTCTCACATGTTTGAATATGTGCACCACAAATTTTGTTAGTGTCATCA AAATGCATGTAATCAACTTGCCGTGTATATAATTTCACACAATATCCGTAAAATTTTG CAATTCCTTATGAGCATTTCATGTCTAGAGATTGCAATGACTTGGCTACAAACATGT TTCTCTACACAAGATCACAATATTTAGTCAGGACACGAATTGCAATGGGGATTCTCA CAAGCATCACAAGTCATCTCCCATGTACTAAAAAATTGTTTAAAT

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:176	Middle	LPZ-115	AGGTGACCGTATAGTGCATATTCAGATTGCAATTACAGACGTATTAGAACCAGATTT TCGCTTCGATACAGCTCATCGAGAGCAACAGAGATCCAGATCAAAAACCAGACACA GTTTAAGAACATCGAAATACCAAGCCCAGGGACAGTTACCAGCATATAGCTCTACC ACCAACAGATTATTACAGAACCAAAACATAAGACCACTTGCAGACAAAAATAAACCC TAACGCAGAACGTGGCAACTATCTCCTCCAGCTACCACCATCGGAACCACCACCAC CATAGCGAGAACCCCACCACCACCATAGCCGCCACCGCCACCACCATAACCACCA CCACCACCACCACTGTACCGCCACTACCGCCATAACCACGGTCAC
SEQ ID NO:177	E,L	LPZ-116	AGGTGACCGTCCTTGGAGATACCAGCTTCAAAACCTCCAGTGGTGGAGTCGATGAT CAA1ACTGCACAGTCAGCCTGAGATGTTCCAGTAATCATGTTCTTGATAAAATCACG ATGGCCGGGGCATCAATCACAGTGCAGTAGTATTTAGTTGTCTCAAACTTCCAGAG TGCAATATCATTGTGATACCACGGTCAC
SEQ ID NO:178	E,M	LPZ-117	AGGTGACCGTATAGTAGGAACTTTAGGTGCTTTGGTGGCACTCTCCAATTTTCATG TCCTTACATACCCCACTACGGAGAAGGGTAGCCCAAGATTTGAACCCAAGACTTCC GGTTCGTGAGACTTCATTTCCACGGTCAC
SEQ ID NO:179	All	LPZ-118	AGGTGACCGTAAGATCAAGAGCACAGAAAGCAGCCATAGCCCCGCCCATTGAATG CCCATAACAATAATCTGTAACCCATCTCTCTGTTTCTGAGCTTTCTGAACTGCTTCT ACAACAGTGGTCGTAAGGTTGTGTTGTGATAAGCAGAGTAAAATCCATAATGTACC ATTGCACCAGCATATTAGGATAGTTGAGATCAAGTGTCTTACAGAATAAATCCTCCA CCCAATTCTGTAGCTCCTTTCTTGAGTACCCCTGAATGCAATTACAATTGCATTGAT ATCTTCTGCCACACCACAAAAGCCTGAAGGCAGTGTTGTACATCAACTATAAGCTCT ACCACCTGAAAACCCCAGTCAAACCATTGCACCTAGAACAAGTCCAAGACATTAGA GCACTCAAATCATCCATA1AGACCGCAGAAGCATATTGCACAAGTATCTCAGCAAGT GTTCGATTATAGACATGGCCA1GGTCAC
SEQ ID NO:180	Middle	LPZ-119	AGGTGACCGTGGGAGGGGAGATTTTTGATTTATATTTCCAATATAAAAGAAAATCTA NGTTGTAAGGACATGGCAAGAGCTCTTATTTCCGGGGTTTTAGCCGTGGCCCGGA GCGGATGAAAGCAAATGTAAGTCACTCCGTGCTTTCTCGGCATTTGGACGCTTCTA CTCTACCGCACTACAGACGGGATTGAACCTCGCATCTCTGAGTGTTTGGTCGTTTA CATGGCGGACTTGTTCCGCACCTCTGCGGACGTCAAATGCCGCGACGATAATCCC TTTGAGAACAGCGATACGGCAGAAAGATCGCCGTTGACGAAGCGAGAAAACTATTG AGACTTGCAGATGTGGAGCTGAAGAAGAGCTTGAGTCGACGGTCAC
SEQ ID NO:181	Middle	LPZ-120	AGGTGACCGTCCGTTCGGGGTGTATTGTCGAACACGTAGGATGGTGCTACGTTGA AACCACCGTTACCTTCTTCGATATGTTATAGTTCGAGTTCATACGGAGGGAATACC GTTTGTAGTGTTATTCAGCACAACCCCGTCCTGATTAAACACCCCCGCAACCAAGG ACGTATTCGACGTTCGGTATTGTTTGACACACTCAAGTTATAACCCTGAATAGGCG CTACCCGAAGTAAGCATTGTACCAGTCGTTATTTTTGCCTTCGTATTGCGAAGGATT TTGAAATATATCCGGACAGGCTGCAACCGATCTTCATAAAACTCTTTCTTAAACTGA GCAAACTGAACAGCATTAGCATTTTGACCCGACCTTTCATCGGCACCTGCTGCACA CCCGCATACGTATTAAAGCTATGTTCGTCTGGCCAGGTTTGCCTTTTTTGGTTGTAA TCAGGACAACGCCGTTAGCCGCCCGCGATCCGTAGAGCGACGTAGAAAGCCGCAT CTTTCAGCACGGTCAC
SEQ ID NO:182	Late	LPZ-122	AGGTGACCGTGAAATATGTGGGAGATGATATGTGGTTTCCTGAATATTCACCTCTT GTGTAGAAAAGTGAGATCCTTAAGATGTTTTGCTAATAAGACTCTTAGGAATGTTGG ACCCCTTTCAGAATGCCATTTGAATAGATTCAAGGTGGTAGCTGTTGCCTGGGGCT GTTTTAGGGTTTTAGGCCATGCTCTGTAATTTCATTGAGTCAAAATTGGATTAACTG GTGTCTTTTACCTCATAATAGCTACTGCAGTATTTGTCGATATAGCTTCCCTATTTAT TGACTCTCCTTAGGTACGGTCAC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:183	Late	LPZ-124	AGGTGACCGTCCGTTCGGGGTGTATTGTCGAACACGTAGGATGGTGCTACGTTGA AACCACCGTTACCTTCTTCGATATGTTATAGTTCGAGTTCATACGGAGGGAATACC GTTTGTAGTGTTATTCAGCACAACCCCGTCCTGATTAAACACCCCCGCAACCAAGG ACGTATTCGACGTTCGGTATTGTTTGACACACTCAAGTTATAACTCTGAATAGGCGC TACCCGAAGTAAGCATTGTACCAAGTCGTTATTTTTGCCTTCGTACTGCGAAGGATT TTGAAATATATCCGCACAGGCTGCAACTGATCTTCGTAAAACTCTTTCTTAAACTGA GCAAACTGAACAGCATCAGCATTTTGACCCGACCTTTCATCGGCACCTGCTGCACA CCCGCATACGTATTAAAGCAATGTTCGTCTGGCCAGGTTTGCCTTTTTTGGTTGTAA CAGGACAACGCCGTTAGCCGCCGCGATCCGTAGAGCGACGTAGAAGCCGCATCTT TCAGCACGGTCAC
SEQ ID NO:184	Middle	LPZ-126	AGGTGACCGTCGTCAGAAAAAACGTGATTTCCGCAAACTTTGGATCACTCGTATCA ATGGGCAGCTCGTTTGAACGGACTTTCATACTCACAATTGATGCATGGTTTGAAGTT GGCTGAATCGAAGTGAACCGTAAAATGTTGGCTGACTTGGCTGTTAACGATGCAGC AGCTTTCAAACTCTTGCAGACGCAGCTAAAGCTAAGCTTGGGTAAATAATTAAAAAA AGAACCGAGGTTTCCTTGGTTCTTTTTTATAACTTTTAATGAAAAGTATGAAGAGAG AAACAGCCTGTCTTCTACTTATAGTATAAGATAAAAGCTTGTTACTGATAAGACAGC TTTCATGGTAAAGCAGTTAAAAATAGGGATTTGCGATATAATAGAAAAAACAGACGT TTATGTAAATAAAAAACAGTAGAATGGAGAAATTATGTCAGAGAATCGTTTGGCTTG GGATCAGTATTTTGCGGCCAGGCTCTCTTAATCGCTAATCGCTCAACCTGTAAGCG AGCCAAAGGTGGCTCCGTATTGTCAAGGATAATAAGGGTTATTTCAACTGGGTACA ATGGCTCAGTTTCAGGGACTGGAGACTGTATTGACCAAGGAGTGCCTGGTCATTGA CGGTCAC
SEQ ID NO:185	Late	LPZ-127	AGGTGACCGTGGCGGAGGTTAGGGAAGTTTGACTTCTCATTTTCTCACGCACTCCT CTCCTCGTAACCTCGGTCGAGTCGATGGCGGCTTTTTAGTCGAGTGTGCTAACGCA CCCTCCGGCCTCAAAATTTCCAGCTACTCGTATTTGATCAATGCTGAAATCGCGTAA TTACGTAGTAATAAAGCGTAATGAATTCTATAATGAAGCATGTTTCTCTATAGTTCAT GTGCCGAGAGGAATAATGAAAATGAGGCCTTATATATTATCTGGGGCTCAAGGAGA TGTTATCTTTTCCTTCCTTGGTTAGAGACCGTCAACCTTCACTTGATTGGATAAAGC TTCATTTTGTTAAAACCTCCAAGCCAGTAGATACATACGGTAGGCACGTATTATGGT AGAGACATACGGTCAC
SEQ ID NO:186	Late	LPZ-128	AGGTGACCGTCCTGTTGCCTAACCGCGAATCCAAATCGACTTGGGCTGCTTCCTTT CGTGCAGATATTTCTGGTTTGGACTCTAGTTCTTGCTCCTGGAAATCATGCTTGAGT GCTGGGTAGCTGCCTCCAAGTTTGGTTGACAGGCCCATTCCTTACAGCTTCTCTCT TCCGCTTATGACAGAGTAATGACAGGAATTCAACCTGACGGATCCGTCTAGCTCTC ACAAGGTTGGGACCCTGTCTTCGAGAGGGTTATTTCTTGAGACTGTTGACTATATTT TGGATGAGCCCTCAGCTCTGTGTACTATTGTTCATGTACTGGATACTTTGTAAATGA TTTTATTCTGGTTTTACCCCGGGGGGGGCATTTTGACTCCTGGGTTTAATACGGTC AC
SEQ ID NO:187	Late	LPZ-131	AGGTGACCGTGGAACATGATGATTAGTTCTTCTGTGGGCCAGGATGATTAGTTCTC TGTGTGACTGTGGGCCAGGATGATTAGTTCTCCTGTGACGACTGTTGGATAGGATG ATTCGTCTCCTGTGGACAGGATGATTAGTTCTCCTGTCGAGGCACCCTACCCATGC AATTTGGGATCATGGGAAGTACCTCTCATCTGATCAATGAGTAGGGAAATGGGGTT AGGGACCATTAGAGTACTATCGATGGACACATCGTTGTATCTACCGTCCTATGCTA GGACGACCTCCATTGTTTGGGATTAGTGAGAGTGGTATGACACTCTGAGACTGACT TTGGGTCAGTGGAGGATGTATGATACATCCTCGATCATTTCTTCTTCTTCATAGTTC GAGCAGAGCAGAGCACAACAGGCCAAGTAGTGCAGGGTAGTGCATTTGATGGCTG GGATAGTAGCGACGGTCAC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:188	Middle	LPZ-133	AGGTGACCGTAAATAAGATGACCCACATGGAGTTTGGCCCTAGTTTCCAATTTTAA CAC1CGCTCTCAACTAGGGAGAACTCCATTCGCTGATCCATTTGTCCGACTATACTA TCTCTGCATCAGTGCCCTACACTACTCTGCACTGCTCTGCTCTACTAAACCATGAA GAAGAAGAATGACCGAGAATGTCTCATGCCATTCTCTATTGACCTGAAGTTAGTCC TATATGAAGAGA1TGTGTCATATCACTCTTATTGACCCAAAGTCAGTTTTATTGATCC CAGATCAATATCACAGAGAGTGTCTCAAACCACTCATACTGATCCCAGATCAGTTTC ATTGATCCCATATCAAGGAGATCATCCTAGAATAGGGAGTACAGTAGATACAATGAT GCATCCATCAATAGTACT1CTATGGTCCCTAACCCCATTTCCCTGCTCATTGATCAG ATGAGAGGTACTTCCGATGAGCCCACACTGCATGGGTAGGATGCCTCGACATGAG AAATAATCATCCTATCCACAGGAGACGAATCCTCCTGTCCCACGGTCAC
SEQ ID NO:189	Middle	LPZ-136	CTAGGGAAGACTTTAAAAGTTTGTAAAACTAAGCATAGCTCTTAAACACTGAAGTTA AAGACATGATTGGAATGTGCAAGTGGTTCAGTATCCAAATATTGAAGGTTGCAGAA TATGGGCTACTGTGCAAACGAGTAACTTTATCTATATTTTCACAAGATCATACAATG GGAAACGTGAGATAACAACTGCATCGGTGAACCAGAATAGTTATAAAAGTTCTTGC AAGTAAAGGGTGAATAATTGCATGGTGTGAATTAAGAATGACCATGTAGAGCTGCT ATACAGACTTCTCAAGGTTTTATATTTGAGGAGTGCGCGCTATTGATGTTGTGCAAA AATTTCAGAAATTAATTCTGCGGCATTTATCAAGGTTGTTTGAGCCATTTAAATAGCA AGTTTTTGTTTCTCCAGTACTTTCAGGAAAGCAGGTTAGACGATAAAATGCATCTTC CCAATTTACTATATTTCTGTTTTAAAAGATTCTCTCAATGTCCTTAGCACGTGGCTTT CATTATTGGGACCAATGAAGATGTGTAGCAGAGGCATTACGTTATGGAATCTCTCA CCAAGAACACTGTTTTGGGCTTTAGATAGCTCCTAGTTATAAATGCTCCAGTGACAA ACACATCCTAAGTTTGGGGCAATTAATGACGCCTTTTGGTCATTCTCCTTTGGGTTT CAGGCACGGTCAC
SEQ ID NO:190	Late	LPZ-137	TCCCTTTAGTGAGGGTTAATAGATCTATAGTGTCACCTAAATCGCGGCCGCTCTAG AACAGTGGATCCGCAAGCAGGATAGACGGCATATGCATTGGATGCTGAGAATTCG ATATCAACTTATCGATACCGTCGACCTCGAGGG
SEQ ID NO:191	Middle	LPZ-138	GGTGCGATCCTAAACATGCAAGCTTTGAGTTTGTAACTTTGTAGAAGTGGACATTTC TAAGTTGGATGTACAAATCTACTGTTGGTTGTATTGTCATCCCATAAACAACTGTTT GATGAGATGTTTTTTTAAAAACCACATCATAATATTTTTAGGCCTTGTAAAAAAAAAA AAAAAAAAAAAAA
SEQ ID NO:192	Late	LPZ-140	ATTCCAAACTTTTCTTTCAAGATGTACACCAACATCATTGTCCCCAACTTAGTAGACT TGACTTTTCACCAGGTCCAAAGAGAGGGGTGGTGGAAGCAGATTTCAGGCTTTCG AATAAGTATCAATGATATAAGCATCATCCCCTTGCCAATTGTTCTGGATCGCAC
SEQ ID NO:193	All	LPZ-141	GGTGCGATCCCATCAGGGGTTGTGTTTCTAAGAATCACTTCCATGTTTCAAATTCAG CACTTGATCTTGTACATACCCAATTTGTTGCCTGCTACTAGCTAGTATTGTCTTTCA GTTTGAACCATTTTTTTGAGTAAATCGTGTTTAGTCTTTGGCAAAAAAAAAAA
SEQ ID NO:194	Middle	LPZ-143	GGTGCGATCCGCATTAGAGAAGCATACAGGAAAAAGAAGTACCTGCCTCTTGATTT GCGCCCAAGAAGACTCGTGCTATCAGGCGACGCCTTACCAAGCATCAGGCATCAT TGAAGACGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATGCAG TCAAGGTGTAAGCCACAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTTGCGGGA TGATATTGCCTATATATTTCCGTCCACGTTTTTGGCAAATTCCGATTTGCATCAGAA TTCAAGTTATGATAGTGTTCTTTCGCTTTTGAGCAGTTGATATTGTTTATCTTTTATT TCTCTTGAATTGCAACATATTCTAATGCAATGAGTGGATTATTATATTGTGGTATTTC CATGTTGAACTCATATAAATGAGCGTAATTTGAGTGGTAGCGCTAGGATATTTACAC TTGGCAAAAAAAAAAA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:195	Middle	LPZ-144	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCTGCAATATAAGGAT GGCTAACTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCAGA GTTGTCAAATAACTTTTGTGAATAGGAAAGTTGTCCTCTTTTAGAGTGCAGAAATCC TGCAATATAAGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCAAAAA AAAAAA
SEQ ID NO:196	Late	LPZ-145	GGTGCGATCCCATATACAATTACATATATTTTCAACAATTCTTTTGTTGTTATGAAAA TCTATTGAAATAAATTGAAATAGTTTGCATCATTTATTTATCGGAATTCGTATTTATAT ATTAAATTTCTGATGTCTCAAATCCTTCGTTACTGTAACGATATCATTAATATAATGT GTCTGCAAGTTTATTGGGCAAAACAAAATTTATTTTTCGGTCACATCATAAGTTTATT TTTGGTCACATCATATGCACCATCACATTAAGCATAAGCATATACAGTAGCGTAAAA ATACAATTATTGTTGTTGACTAGGATCGCAC
SEQ ID NO:197	Late	LPZ-146	GGTGCGATCCTAGTCAACAACAATAATATGTATTTTTACGCTACTGTATATGCTTAT GCTAATGTGATGGTGCATATGATGTGACCAAAAAATAAACTTATGATGTGACCGAAA AATAATTTTGTTTTGTCCAATTAGACTTGCTGTATATGTCTGGAGTCCTACCCTTGAA AATTGACTTGTTTCCC
SEQ ID NO:198	Late	LPZ-147	GGTGCGATCCCATATACAATTACTTATATTTTCAACAATTCTTTTGTTGTTATGAAAA TCTATTGAAATAAATTGAAATAGTTTGCATCATTTATTTATCGGAATTCGTATTTATAT ATTAAATTTCTGATGTCTCAAATCCTTC
SEQ ID NO:199	Late	LPZ-148	CCACTGCACCATATATTTTCATATAGCTGAAAAACTTAGCCATCCTTATATTGCAGAT TTCTGTTTTCTGAAACAGGAATTACAGGATCCATCACTGTACTCCTTTGCCTTCTTT GCCGTTCATCATCCAAACTACCTATACGGATCGCAC
SEQ ID NO:200	All	LPZ-149	AGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATAAAAATTCCCAGTT TGAATTCTAAAGAAAACTGTTCAATATTTGAAGGCCTCTGATATCACAGAGACTGAT ATTAAATGGAAATTCATACAAATGAGGAGAGCATGTAGCAACACTAGAAGCTTTGG CATAAAGCACCAGATAAATTCATAAGAACTAAATCCATAAGAAGGATCTCTCGTTCA CCAGTCACAATCACACTCGGATCGCAC
SEQ ID NO:201	Middle	LPZ-150	GGTGCGATCCCTGGCCCTGATAACTTTGGTTGCAATGGAAAATGCAGTACTAGGTG CGAAATGCTAAAGCCCGCCCGGAGCGGTGCATGAAGTACTGCAATATTTGTTGTAG TAAATGGCTGGTTGTGTTCCCAGTGGTCACTATGGCAACAAGGACGAGTGCCCCT GCTACAGAGAATGAAGTCCGCAGCCGGCAAGCCCAAGTGTCCCTGATCTTAGCAC TTCAGTCCAGTCGCCACTTCTTTTATTCTCTTTTTTTATAAAAGTGACGAGGCCGTTT TTCTTGTGCTTGGTGCCATATGTAGAGCGGTGGCTACTTCTCCTGTGTTAGGAAAT GTTGCAGTACTAATAATAGAACTTCTT
SEQ ID NO:202	Middle	LPZ-151	GGTGCGATCCAATAAAGATATACTTTGCAACAATAATCAAAATATCATTATGCAAAG TTTAAGATCAAAATAGAATGCAACAAAAAAATGGTTGTAACATAGGAACCAACAATG TTGCATTCAAGTAAGACTCTTTGCAAAAAAAAAAAATAAAAAAAAAAA
SEQ ID NO:203	Middle	LPZ-152	GGTGCGATCCACAAGTAAGATAATTGAGTATATATTCAAGATGCAAATATTTCATTA GGACCACTCATAAAGTTATCAATGATTCACAAAGAGACCTCCTGACCTCTCTCAAAA GTGGTGGCAACACAAGACTAGTGTAGTTTTTACTATACCTCAATGAAACTACCATCC TAACTGATGCCATAATCTTCTGTTATATATTACCAAAATTTATGAGATGATTGATCCA TAAACACTCCAGAACACATAGTCATCCAAAGGAACCTTTGCTTGAATATGGACCCC CTTAATTCAGGTACTTGCTACTCCAATAAATTGCTTAATCTCTCCACCGATAACCAC AGTTTGGATCGCC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:204	Early	LPZ-153	GGTGCGATCCAGGACATGAGGCCGAGTTTGCCATTGTGATATGATTGAGGAAGTC CAGTCTCAAAATTAGGTTTATCTTGATGTTTGACAAGAAATATAGAAGGGCATGATG AATCAAGAACCTTTTCCAAATCTGTTACTGCAACCAATCCAATGACATAATAACGCC AATGGTTGGTTCCTGTGATGACATAATAAATTGGATTAAATTAATAACATCCCTAATG CCATGTGGTTAGCTGCATCATCACCGTATCCATCGAGTGTTCAATTTTTGGGATGTA TGTATCAAAAAAA
SEQ ID NO:205	Early	LPZ-154	AAATATTTTTCAATACAACGCCATGTGACATTTTTGTGCTTCTTGTTTTTGATACATA CTTCCAAAAACTGAACACTCGATGGATACGGTGATGATGCAGCTACAGCCATTGCA TTACGATGTTACTAAATTAAATCAATTTATTATGTCATCACACGAACCCAAACAATAG CGCTATATGTCATTAGAATGGTTGCAGTTACAGATCTGGAAACAGATCAATGAATCA TCATGCCCTCTATATCTCTTGTCAAACATCAAGATAAACCTAATTTTGAGGACTGGA CTTCCTCAACATATCACAATGGCAAACTCGGCCTCATGTCCTGGATCGCAC
SEQ ID NO:206	Middle	LPZ-155	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCTGCAATATAAGGAT GGCTAACTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCAGA GTTGTGAAATAACTTTTGTGAATAGGAAAGTTTTCCTGTTTTAGAATGCAGAAATCC TGCAATATAAGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCAGAGT TGTCAATATAAACTTGTGAATAGGGAAGTTTTGGCAAAAAAAAAAAAAAGAAAAAAA AAAA
SEQ ID NO:207	Late	LPZ-157	GGTGCGATCCTCGTTGTGAAGACGTAGTGATGGAAAGGTCATGTTTGTAGGAGAC ATAATTATAGGAGTTTCTTTATTATAATAACCAAGAAGTCCGATCCTGGGGGCGTTG AGTATATAGTCAGTCTTTGGTAATTTGGTGTGGTGCTGTTTGACCTGCCTTTCCTTT GGAGCAATGATCCTTGAGGATGGAAGAGGTTATGTTGAGGCTCAAGAGATGATTGT TTGAGTTGTGGAAAGCAAAAGGTTTCCAGATGTAGTCAGATAGTAACTTCTATGCTT TTAATAAAATTTAGTCTGTGGGGCATGCCCCTTTTTGCTGGCAAAAAAAAAAAAGAA AAAAAAAAAA
SEQ ID NO:208	Late	LPZ-158	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGTGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCTGCAATATAAGGA TGGCTAAGCTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCA GAGTTGTGAATATAACTTTTGTGAATAGGAAAGTTTTCCTGTTTTAGAATGCAGAAA TCCTGCAATATAAGGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCA GAGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:209	Middle	LPZ-162	GGTGCGATCCCAGGAGAATATTAGTTTCATGTGTTGCTATCATTTTCTTCAATATGC AGGGCAACCATTTGAATGAAACTATTCCTTTCGAATTTCAAAAACTTAATAGGCTAA CTTATCTATCTGGAGCCGATTTTCATTGACGAGTAACCTGTAAGCTGGCCAGCAAA AGCCAACAGATGTTCAGCTTGTTGGAACCAGTTGAAGATTGTAATAGAGATGGTGA ATAATCGCGGACGGCTCGGCCAATGGAATATTTGTTGCATCATCATCAAGGGGGTA TGAATTCCAAAGAACTTGTTGATTGAAATTCCCAAGCAAAATTCTGTGAAATGAAAA ATTTATTGAGACCATTGGGCAAAAAAAAAAAAAAATAAAAAAAAAAAAAA
SEQ ID NO:210	All	LPZ-165	GGTGCGATCCGACTGTGATATGTGACTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTCTAGGGTTGCTACATGCTTCCATTCTAATATC AGTCTCTGTGATATCAGAGGCCTTCAAATATTGAACAGTTTTCTTTAGAATTCCAAA CTGGGAATTTTTATTGTATAGCCATGTTTTCACGGATTGTCTGCAAGAAGGCTCTTT GGCAAAAAAAAAAAA
SEQ ID NO:211	M,L	LPZ-166	TTTTTTTATTTTTTTTTTTTCCAACGAGATCACTGTCATTGTTCAATAACTATATGCCA AAGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATAAAAATTCCCAGT TTGGAATTCTAAAGAAAACTGTTCAATATTTGAAGGCCTCTGATATCCCAGAGACTG ATATTAGAATGGAAATTCATACAAATGAGGAGAGCATGTAGCAACACTAGAAGCTTT GGCATAAAGACACCAGATAAATTCATAAGAACTAAATCCATAAGAAGGATCTCTCGT TCACCAGTCACATATCATACTCGGATCGCACC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:212	Middle	LPZ-167	GGTGCGATCCGACTGTGATATGTGGCTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTTTAGGGTTGCTACATGCTCTCCTCTTTTGTAT GAATTTCCATTCTAATATCAGTCTCTGTGATATCAGAGGCCTTCAAATATTGAACAG TTTTATTTAGAATTCCAAACTGGGAATTTATTGTATAGCAATGTTTTCACGGATTGTC TGCAAGAAGGCTCTTTGGAAAAAAAAAAAATAAAAAAAAAAAA
SEQ ID NO:213	Middle	LPZ-169	TCCCAAAGGCAATTATACATGGATCGCACC
SEQ ID NO:214	All	LPZ-170	GGTGCGATCCCCACTGCAGAAAGATGAGCCAGTACCCTGAAATTTTGCTGTTGTCC ATGCCTGGGTCACGGAGGAAAGAACGGCACGGTGCAATATGATTTTGCTACATACA AGTTCCAAGAGTGGATGCAGACAGTGCTGGCCATGGCTGATTATTTGCAGGTGACT AATGCTCTTTTGGTTATCCTTACCATCATCATCTTCCTGCCATTCTTTTGTACCTCGG TATGGAGACGAACACCCACTTTTCAAAGTTTGCAGAGGAAGCATGTATTCATAACA GGAGGATCAAGCGGCATTGGCCTTGAGATTGCCAAAGAGGCTCTTTCACAGGGTT CTTACGTGACACTGGCGTCAAGAAATCTTTCTAAACTTCGTAGGGCTGTTGAAGAA ATCATCCAAGAAGTGGAGTGCGACGGAGACAAGATTAATATCAAGGTAATATACCC TGCAAAATGTTGTCTGGAATACAATCCAAAACCAATTTAGCAATTAACCCATTGGCA AAAAAAAAAAA
SEQ ID NO:215	All	LPZ-171	GGTGCGATCCAAGTGCGGTATTCTTCCTTTGGCAGTTCTCTGAACTGTTGAGAGAA TTTGAGTAGGATAACGACAATAATTACTATGCTCACAAGCCCAGACAACACGAATAG ACTCCCTTCCGTGCGTCGCCTTCCAGAGGACGCAGCAGCTAAAATCTCGGCCTGA CTCACCACATATATATTTAATAGCTTGTATATGCCATATGAACTGTTAGCATGATCTC CCTCTAACTGCGAATTGTGTTGCTGTAAACTAATCCCAAAGGATGTTTACTCTGTTG CTTTTCCAACTGCTGATGGATTTCGCTCATACAATGACCCGAGAGCACCATAAACCT ACCCAGCGTTGTGGCCTATGACCCATAGCTTTTTGTTCGCACAGCAATTGAAGACC GGCTACAGGAGATGACTAATGCACTTCCGAGAAGGTTTCACCGCGAATGACAGGG AAGGACAAGGCAGAGCAGCAGGCCAAGACAGCTTTAGTCGCAGAAGTTCAAGCAG ATCTAGATTCATAGTAAATGGAAGTTCTACACTAGTTACAAATTTAAAAACGTACCTG CATGGACTACACGGTTTATTTACGAGTGCCACTTGTCTCATTGTTTTCCATCAGATG TCTGCTGGATTGTGGTAGTGTGTTCTACCGTATCGGTGCGGGTTTTGTATATTGTG CGTCGACAGAGTGACAGGTGGTGATTTTACTGGCAAAAAAAAAAAACAAAAAAAAA A
SEQ ID NO:216	Late	LPZ-172	GGTGCGATCCTAGTACAGGCGTTTGGAACAGAGTGGAGAATATGTGGAGTATTGG GGGATGCCCCCGGTCGTGTGTTGCTGCGTTTGGGAATTTGTATTTCTTCCATAGGC AACAAGTGATGTCTTATAATAGTAAAGAGAATGTTTGGGAAGTGGTGGCATCTCTTC CTGGAGACATGAATATTGTTACTTTGCGCAACAGTGTGGTGTGACAAGATATTTGT GAGCGGTTGTGCTTGCAGTGGCGGCGATCAGGTGTGTTACATGCTGGACAAATCT TGGGCGTGGGCTCCTATTGAGAGGTCACATGAGTTTGAGGGTTTTGCTCAGTCTG CAATAACTGTAGAGATATGAGCAAATTCTGTTGGGTTCACTTAATTTTGGGATTATT ATAGTGCAGAGGGGAGCCGGGAAGTTTCAGTGTACAGTGATGGGCACCACATGTT GCCAGCATTGGGGGTGCCCTGTGAATATGATTTCTATAAGTCCGGATTTTAAATATC TAGGCCATCTATCTCATCCAGCCTCTGATTGTGTCTGTACTAAATATATCCTGTATA TTCGTGATCCCTGGTTTTGAAGTGAGCAAGTTTTAGTGGAAGAGGATTTTTATTAAA TATATATAAAGTTTCTGTATTCAGGGTTTTGGCAAAAAAAAAAAAAA
SEQ ID NO:217	Middle	LPZ-173	GGTGCAATCCGCCATAAGAGAGGCATACAGGAAAAAGAAGTACCTGCCTCTTGATT TGCGTCCCAAGAAGACTCGTGCTATCAGGTGACGCCTTACCAAGCATCAGGCATCA TTGAAGACTGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATGC AGTCAAGGTGTAAAGCCATAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTTGCG GGATGATATTGCCTATTATATTTCCGTCCACGTTTTTGGCAAATTCCGATTTGCATC AGAATTCAAGTTATGATAGGTGTTCTTTCGCTTTTGAGCAGTTGATATTGTTTATCTT TATTTCTCTTGAATTGCGAACATATTCTAATGCAATGAGTGGATTATTATATTGTGGC AAAAAAAAAAAAAAAAAAAAAAAA

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:218	Middle	LPZ-174	GCGGACGCCTCAGGATAGCGTTAGGGTTGCCTTAGGATAGCGTTAGCTCTGCCTT CTAAGGTTGCCGTCTTATCCTCCAGCGTCTAGGGCTTCCACTCCTAGGATTTCTCT TCCACTAAAACCCAAGACAAGTGGAGAGAAATCAAGATAGAAGTGTGTGTGAAATG ACTCTTAAGTCATCTCCTTTTAGACTAAAACATTGAGCACATGTGGGGTTTATTTGG TTGCTGGCCGTCGTT
SEQ ID NO:219	Middle	LPZ-175	GGTGCGATCCTGAAACAACATATTCCCGATGGCTCTTCCGAAGGAACCATTGCTCT ACTGTGTGGCCCTCCCCCCATGATCCAAGATGCCTGCCTACCTAACCTGGCCAAAA TGAATTATGACATTCAGAATTCGTGTTTTCAGTTCTAATTACACCCTTCTGGTTAATC AAATTGGGACATCCCCTCCCACATCCTGTTATTAATTAAGCCATAGTCTAGTGTATA AAATCTGTTGATGTGTACAGCATCAAGTTAATTTCCTCCTTTTCTGTCAAAAAAAAAA AAAAATAAAAAAAAAAAA
SEQ ID NO:220	Late	LPZ-177	GGTGCGATCCGATCCTAAGCGGGTGCATATATATAATGACAAGCTGTAGTAACTAA CTCTTGTCATGAGGCCATTGCTAACATAGCCTGTCCAATGCACATAGCAGTCAAAA AAAGCAAATAGCCGCCATGTTCCCATACACGAAGTAAGTACCCTCCCTATTGAGTC ACCTTACCCGCCGAGAGAGATCCCAATTCCATGTATTCGGTTAAGTAAGCCCTGCC AGCTATGTCCCACCCATGAAAGAAAGTACTGATCCGAGTGGATCGCACC
SEQ ID NO:221	Late	LPZ-179	GGTGCGATCCAAACTGTGGTTATCGGTGGAGAGATTAAGCAATTTATTGGAGTAGC AAGTACGCTGAATTAAGGGGGTCCATATTCAAGCAAAGGTTCCTTTGGATGACTAT GTGTTCTGGAAGTGTTTATGGATCAATCATCTCATAAATTTTGGTAATATATAACAGA AGATTATGGCATCCAGTTAGGATGGTAGTTTCATTGAGGTATAGTAAAAACTACACT AAGTCTTGTGTTGCCACCCACTTTTGAGAGAGGTCAGGAGGTCTCTTTGTGAATCA TTGATAACTTTATGAGTGGTACCTAATGAAATATTTGCATCTTGAATATATACTCAAT TGATCTTACTTGTGGATCGCACC
SEQ ID NO:222	Late	LPZ-181	CAATCTGTCTGCAATTGATATTATTGCATCCAGTAAACCAGATACACATTCACCACA ACATTAGAGACTCTAGAAGTTCCTTTGGCGACAGGCAAAACTCATGATTACAGATAA TTGGAGTTTCCTCTAACCAGAGTCAAACGATCTAAAGGGATTTGTCTAGTCCTCCAT TCCCTCATTCAATGAGGCGATGGCTTATGCCGTGACAACAGTTTCTATAGTTGCAT CCGCTCCTCTTGATCCCACAACATTTTTGGTGTTCTCTGCATCTTCTTCCTCCCATA TCTCTGGCAGGGCTTCTCTAATGTTGTGAATACTTGCAAGGGCAAAATCTGCTCCC TCTGTTCGGATCGCACC
SEQ ID NO:223	Late	LPZ-182	GGTGCGATCCTCTCAGTTACGAGCTCAATTTCGACCAGGGGTCTCGGCAAATTGA GGATCATGAGAAGCAGGGTATGCCCTTGAATGCCCTGAAGCCAGGGGAGTCTCAG GGCAATCACGAATGAAACCTGACAAACCCTAAGAAAACCCCTAGAGCGTGCCCTGC AGAAAGGGAATTCTTTTTGAGGCCGGCGGTCTTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:224	Late	LPZ-186	GGTGCGATCCAGCAAGAGAACGAAAAAGGTATGAGAATCTATGAAATATTTGTACA TCACTGTATTCATATGAGGGCCTTTTTTTACAATGCGGTAGGGTTGTTTGGAGAATT AGAACCTGATTAAAATGTAGATGGATTCAAGCTTTTAGTGAAATGAGGCTCGGAAC GCAAGTATGCTGTCCACTTTGAGACTCATTCTTCTATAGTATCTGAAGCCAAAGCC
SEQ ID NO:225	Middle	LPZ-189	GGTGCGATCCCATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTCACAACTCTGCTGCACCATATATTTTCATATAGCTGAAAAACTTAGCCAT CCTTATATTGCAGGATTTCCGCATTCTAAAACAGGAAAACTTTCCTATTCACAAAAG TTATATTCACAACTCTGCAACTGATATGAGTGCCACTGCACCATATATTTTCATAGC TGAAAAGCTTAGCCAGCCTTATATTGCAGATTTTCTGTTTTCTGAAACAGGAATTAC AGGATCCATCACTGTACTCCTTTGCCTTCCTTGCCCGTTCATCATCCAAACTACTAT ACGGATCGCACCA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:226	Late	LPZ-194	GGTGCGATCCTGCGAGAGCCGAGGGTTCATTTTCCTTTCGACAACGACGTTCAGT GGCGACCAGAGTTTCCCAATCACTTCAGCGATTCTATTCCTTCGTTGTAATAAAGCT TAAGGAATCCATGCTTTATTCCTTGGAAGGTTTGAATATTTATATTTGTTGGCATTAA TGCTATATACATCTATACTAATTTTGGGTTGTTCTAAACTTGTTTTGAATAACTTAAAT
SEQ ID NO:227	All	LPZ-195	GGTGCGATCCATGGCAAAGAGCTCGTTCAAGCACGATCATCCTCCAGAGAGAAGA CAAGCTGAAGCTTCTCGGATTCGAGAAAAGTATCCGGACAGGATTCCGGTTATTGT GGAGAAGGCTGAGAGAAGTGAGATACCTGATATTGATAAAAAGAAATATTTAGTCC CAGCAGATTTGACTGTTGGGCAATTTGTTTATGTTGTCCGAAAAAAAAAAAA
SEQ ID NO:228	Middle	LPZ-196	GGTGCGATCCCCTGTATTCTTGAAAGGGTTATAACGGAAGATAGCATTTTGCTCAG ATTGTAGACAGTCTGCATGATTTGTCAATACTACTATTTCGCATTATTTGTTAATACT ACTAATCCTTGTACTCATCTAGACTATTTAATTATTAAATTCTACAGTTTCTTTCTCCT AGATGGCAAACAATATGAATAAAATGCCAATAGTTTTGGAACTACTCCATTAAGAGC TTTAGATGATTATCATTCATCATTTGCCTGTTTTGAATCGTAAATGAATGTGTCACGG TCTTCTTTTCTGTTAGTCTCTATGCTTTCATCAGAAGAGTCTAAGCCAGTTACTGGA AGCTATTTGTCATCTCTTTAAACATTGTTTCCGTGCCAAAAAAAAAAAAAAAAAAAA AA
SEQ ID NO:229	Late	LPZ-197	GGCAGAACTTCCAAAGTCTAGTATTTGATTAACTAATATGATGAAGACACTCAGTCT ATAACATGACGCCAGAAATCAGACCATATGCATGATAACTAGCACGATTAAAATACA ATTCGCAACCTTTAATACACTAAAAACGTTTACTGTATAGTCCACTCAGAACATTTC GATAGTATTGTCAGATCGACTTATTTAGCTCATATTCAGCAATCTGAACTGTACGAT GCGGCTCATTCAAGGGCATTTGGGTTTGCCCTTGGCATTCTTCATATCCCGATAGC AAGGACACGCGTTCTTGTTGCCATATGTCCCTGGGGGATCGCACC
SEQ ID NO:230	Early	LPZ-198	GGTGCGATCCACATTGGCCAGGCCGGTATTCAGGTCGGCAATGCCTGTTGGGAGC TTTACTGTCTCGAGCACGACATTCAGCCTGATGGACAAATGCCAAGTGACAAGACC GTTGGCGGTGGAGATGATGCATTCAACACATTTTTCAGTGAGACAGGTGCCGGTAA GCATGTTCCTCGT181GCCGTGTTTCTGGATCTGGAGCCAACTGTCATTGATGAAGT TCGAACCGGCACATATCGGCAGCTTTTTCACCCAGAGCAGCTGATCAGTGGCAAA GAAGATGCCGCCAACAACTTTGCTCGTGGCCATTATACCATTGGTAAGGAAATTGT GGATCTGTGCTTGGATCGCACC
SEQ ID NO:231	Late	LPZ-199	GGTGCGATCCCAGCATTGGATGCATTTCTAGCACAAAGCCATCTTGACTAAAATAG CACTGCGGGCAACTGCAGTCCATAACTTTCAGAGCATTGTTGCTGCCTCAATTGTA TACCAATCCATATTCTAAAAATTAGACCTGGAAACCAGTCAGAAATTTAATGTTTTCT TGCAGAAAATGCCCTTTTAGAAAAAGGAGAGAATAACTGCATTCAAGTTCTAACTCC CAGACATAGCCTGGCAACGTCATTCATTCAGTTCGGATCGCACC
SEQ ID NO:232	E,L	LPZ-201	GGTGCGATCCAGAAAACAGCACAAGCAATCTGTAAGACCAATATTATTATCATCTCT CACTGCTCGTGAACAAAATGCTGGTTCATAGCCATCACGAAGGCTAAGGCTACTAT CCAGCCAAACTGATCTCCAACAATAATTTCATAAGCTTAAATAAATAGTCCATCCAG TGGATGGAGCCAGAAAGCCATAGAAACTTCAAATACTTGTGGTATCAATCTCTCCTC TGTTAAGGGAGGTATCAGATCAGAAGCACTAATCAAATGCATACATAAATGCAGTA GACTGCAATAAAACAAAATCTGCAGATAGCAACTGAGCGCTTAACGAACGGAAAAG AGTTTAACTTGATCTATCACAGGATCGCACC
SEQ ID NO:233	Late	LPZ-202	GAAAATGGGAGCCTCAAATATTCAAAGCCTCATCTCAAGAGTCTCAGATTCGGATT CATTTCATTTGGTTCGTAATAAAATAATGCATCAAATAGTTATTATCCACAAAAATGG GAGAATTATTACAATCTGTCTTCTCAACATAAAGTCATAGCATAGCATAGAACCACA CCACAGTCGTCATCATTTGTTTTGTTCACCACCGAAGGGGCTCTTTACAGCGTCCA TGAAGCCCTGTGTAGCACCCTTCGCCTTGTCCCCCGCCTGTTGGAAGAAAGAGCC AGTTTGTTCTTTCCCCTCTTGGGCTTTTCCCGTGATGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:234	Late	LPZ-203	GGTGCGATCCTATTATAGAACCATGACTCTTGTCGATGGGGCATAAACTTCTCATTC TTAGGCGTGCCTACTGTGACTCTTGCCGATGTGGCATAAACTGCTTATTCTTAGTT GTGCCTTCTGTGCAGAACTTGTTGAGTCGGTGGATTACACTGAC
SEQ ID NO:235	Late	LPZ-204	GGTGCGATCCATTAACTAGATTAACGATAACATTCCTCTGCATCCAATCCAATGCTC ATCTAAATCTACTTCTACTTAGATCTCTGCCTCATCTTTCTCCACCTCCTCATCCATT CTGAAATATTAATTTCTGCATAGATTTTGTTAGGGTCTAGTAATCATTTTCATGAATT TAAATCTGTTCTAGTCTCTTATTATTATGCTGCTTATGCTAGCATCAGAACCTGTGTA TAATTCATTCATGTATATATTGGATTACACAAATTATACGGATGCCAGAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:236	Late	LPZ-205	CTTGAAGCTGATATGTTTGAACCCGAAATTTTGTTACCCAACTCCAGTGTACATTGT GTCACTGTCAAAGAGAACATGAGAGCTGCATGCAAGCTTTTGCATGATAGATAGAT TACTGATCACCGAACATTTCTTACTCTACTTTCCTCTCCTATCCCCAGTGATTTTTG GGCATTTTCTATACCCTTCGGATCGCACC
SEQ ID NO:237	Late	LPZ-206	CTCATGAACAGCAATATGATGCATTCCTCTTATACACATTTCATATATGTTCACCCTT GCCGTCATGGCTACTCTAAGAAGAGCAAAACAGACCCATTGAATCTTTACACGCGC TTGTTTATATGAATACAAATAATTTAGGCGTTTCTTTACACGCCCTTGTTTACATTAA TACAAGTGATTTAGGCGTTGTTACCAGAATAGTGCCACGGATCGCACC
SEQ ID NO:238	All	LPZ-207	GGTGCGATCCCAAGATAGAAAAGGGAACTATGGTCTCGAGGAGTGTCAGGTGCTA CAGATCACAATATACATAAGGGTCTGATAGTAGTACTCGGCCCAATGTTTGAGGGC TCTAACTAAGGAGGATCAACCGTACCCTTAGCCGTAAAACCCGACTACCCTATCGT ACGGGCGAGTAATCTCTCTGAGTGTTGTTCTCGGTGTATCGTAGCAGCAACACGG CTGACGGTTTATCTATGGTGAGGTTTCAAAGGAGCTAGGGGGCTTCCAATATACCC AGAGGGTACTTGGAAGACAGTTTATACGCGGTTCTGTCTAATGCGCTACTACTCGA AGGGGTACCCACAGGGGTTACAAGAGAGTGCAACAAGCATGACCACCCCTTGTAT TTCTTGCATGTATGCCTCCCCAAATCCGCAGGTTTATGCGCTCATTGACAGATTCC GTGGTTTAAAGATGCCGGAACATGTCTCTAGCCAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:239	E,L	LPZ-208	GGTGCGATCCTCCTAACCTGCAATGTCCTTCCTGCAACCTGCAATTATTCAACAGA AATTAGGTTTATTTTTCTTTTTGTCTTTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTAAGTAAACGACCATTTCAAACGCCATTTCAAATGCTATGAATTAATGTT GAATTAATGTTAGCATTAAGTCTTAAACATTTTATGTTAAGGCATATATATCGTTCCA ACTACTCTTACAATACACCTGCGGTGTACTCCTGCCACCGCATGTACCACCGTTAC ATGTACGCCTGCCAGCACATCTAACAGGTGCCAACTCCTTTGAACTCATCGTCGCC ATTTTTGTATGCATATTTGAACTCATCGTCGCCATTTTTGGTATCTTCACATATGGCC AGTCCAGGATCGCACC
SEQ ID NO:240	Late	LPZ-210	GGTGCGATCCAAGGAGTGGGCGTGCAATGCGTCGAAGATAGCCACCACTGCAGG GGCGTGGCATGCTGCCGTGCTTCCCACAGGGAGATCAACACCTGCACCTCCGCCT CCTTCCGCGGTTACCACGAG
SEQ ID NO:241	Middle	LPZ-211	GGTGCGATCCAGCCACAGAAAGATTGGTTTACTCGATAATTGAACGGTAGACTTTG TGCAGGTTTAGATTGTGTACATGCTGATCAGTATTGTCTACACCATTTTCAATCTTG TTTAGTTCTATGGTAATTTATGTAACAAATTCAGCGATGTTGGGGAAATTGGTCACA TCAGCTTTGTGCCTATATATTTCAAGTAAATCAGGGGATCCATTAATACTGCTTTTAA AATAATTGGGGCAAAGTTGTGGGATGACTGCTTCAGCGGAATACGTGCTTTTCATA GTGCTGTATGACATTTTGTTGAATATGAATTTTCTTTGTGATACAGTTGCGCGAAAA AAAAAAAA

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:242	Middle	LPZ-212	GGTGCGATCCATGCCAAGAGGGTGACCATCATGCCCAAGGACATTCAGCTCGCTC GCCGCATCCGTGGAGAGAGGGCATAAACAGTCAGTCAGATCCAATGGTGTGTTTT CACACCACCATATGTTTCTTTTACTAAATTTGTTAGGTCCCTTCGGTGGGTCTTTTC TTTCCCCCGATTTTAGTATTTTGTTGTTCTTCTGAGTTTCATCATTGCAAGTACAAGA TGCAGAATTGATGGTTATTGGGACTTGGAGACTGGTTATTGCTATGTAGAGTATTTA TATTAGACAGGTTTCACTTGAAGATATAAAATTG
SEQ ID NO:243	Late	LPZ-213	GGTGCGATCCTCATGTGTTATAACCGAAGTTTGCGGGATTCAGATGGTCAGTATCT TAAATGTCCAACTTTCGGTACGAATGGGGTGCGTTCTGAAACGTGCCACGAAAGAG GTGTTCAGGATCTGTCTGAGGCATCTTTCCGGTATTTTCCACTTCCATGGTATGAG AAACTTTCGTCTTGTTGCAG
SEQ ID NO:244	Late	LPZ-214	AGGAGACACAACTTTACGAAAAAGTTCAATCTGGAGTCTTCTAAGTTTTTCAGACTC TCTAAATATGAAAAGCGCCGAGTTTCTCCTATACTGGACTCGTTAAAATTTTACAGT AAAGGACCTGTTCTATTACAAACAGGAACGGACCGCTCCTCCTTAGGGATCGCACC
SEQ ID NO:245	Late	LPZ-215	GGTGCGATCCAGCAAGAGAACGAAAAAGATATGAAGAATCTATGAAATATTTGTAC ATCACTGTATTCATATGAGGGCCTTTTTTTACAATGCGGTAGGGTTGTTTGGAGAAT TAGAACCTGATTAAAATGTAGATGGATTCAAGCTTTTAGTGAAATGAGGCT
SEQ ID NO:246	Late	LPZ-216	CTCAACATAAAGTCATAGCATAGCACCACACCACAGTCGTCATCATTTGTTTTGTTC ACCACCGAAGGGGCTCTTTACAGCGTCCTTGAAGCCCTGTATAGCACCCTTCGCCT TGTCCCCCGCCTGTTGGAAGAAAGAGCCAGTTTGTTCTTTCCCCTCTTGGGCTTTT CCCGTGATGGATCGCACC
SEQ ID NO:247	Middle	LPZ-217	GGTGCGATCCCATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTCGGGACCAAATATTTTTCAATACAACGCCATGTGACATTTTTGTGCTTCTTGT TTTTGATACATACATTCCAAAAACTGAACACTCGATGGATACGGTGATGATGCAGCT ACAGCCATTGCATTACAGATGTTATTAAATTAAATCAATTTATTATGTCATCACACCA ACCCAAACAATAGCGCTATTATGTCATTAGAATGGTTGCAGTTACAAGATCTGCAAA CAGATCAATGAATCATCATGCCCCTCTATATCTCTTGTCAAACATCAAGATAAACCT AATTTTAGGACTGGACTTCCTCAATCATATCACAATGGCAAACTCAGCCTCATGTCC
SEQ ID NO:248	Late	LPZ-219	GGTGCGATCCTGGACTGGCCATATGTGAAGATAACAAAAATGGCGACGATGAGTTC AAATATGCATAGAATAAGCGTTCTGTAATTGGAACGGCCATAGGAGTTGGCACCTG TTAGATGTGCTGGCAGGCGTACATGTAACGGTGGTACATGCGGTGGCAGGAGTAC ACCGCAGGTGTATTGTAAGAGTAGTTGGAACGATATATATGCCTTAACATAAAATGT TTAAGACTTAATGCTAACATTAATTCAACATTAATTCATAG
SEQ ID NO:249	E,L	LPZ-220	GGTGCGATCCCATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTTTTGTGAAGTGACAAAATCTA AACCAAAGATTAAAAGGCTTTGGCTTCAGATACTATAGAAGAATGAGTCTCAAAGTG GACAGCATACTTGCGTTCCGAGCCTCATTTCACTAAAAGCTTGAATCCATCTACATT TTAATCAGGTTCTAATTCTCCAAACAACCCTACCGCATTGTAAAAAAAGGCCCTCAT ATGAATACAGTGATGTACAAATATTTCATAGATTCTCATATCTTTTTCGTTCTCTTGC TGGATCGCACC
SEQ ID NO:250	Late	LPZ-221	GGTGCGATCCCAACCAGGTGTCCATGCAATATATGGTGAGCATCAAGTTTGAGGTG GTTGATTGAAAGTTACAAATTGGTGACATCTGAAGTCTCATTCAGTTATGTTTTTGTA TATAAAAACCATAACCAATTTTGTATATAAGATCCATAATCAATTTTGGCCAA
SEQ ID NO:251	Late	LPZ-222	GTTTTCAAGAAGAGCCTGACGGTTTCCTCGGCGGGATGACGGAAACAGGAAGCGG CCGGCCGGTTCCGGACCCTCCGCAGGCGGAGCATAGCATTTTGCCGGAACCACC GCATGTCCTGCACCCAACATCCGCGTCTGACCAGCGGAGGCACATGCACCCAACC CTCCCGGTTCCATTGCACCTCGGGCAGCGCGGCCACCCGCCGGCCATCGGCTTAT CCATCATGGATCGCACC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:252	Late	LPZ-223	TGGGCGAATCATATGGCTTGCATTTTCATTGTAACATGTATACGTTAAGGATTATCA TAATGCCTCCAAAACCTTGTATCTTCGTCCTTGCCACAATACATCCAGGATAACTAA TGGAAGCTTGACATGTCTTCACCAGTAATAATATATCAACTATAATACATGCCATTCT TTTATCAGTTTTGAACAAAATAATCGATTTGCATTCTTGACAAAGAACCTCGCGCAT AAAAACAAATAAATTCTCATAATGCCTCCCAAACCTTGTAGTCTGGGCCCTCAGTCG CCACAATCCATTTAAGAGGAATTTGGGGGTTGATAGTGCCCAGGTCCAATCTTCAT GAAAATTCGTTCATCAATCTTTGCTGCATACACATCTCTCTCTGCTTTCACTATCTG GGATCGCACC
SEQ ID NO:253	Late	LPZ-224	CCACTATAATGAACATTGATATTACAAATATAATATACATTAATATTACAATTCAAATC ATTGACAATGAGCAGGCACTACTTGCAGTGCTTTGGAATTCAGACTTCTGATTTGCA ATTAATTCTTGTAGACGCTTTTCTGGGAGGGCAGGTTTTCCGCTTCAGAGAAAACC ACGTACAAAACGATATTAAATAAAAATAGACACATACAAAAAATACTTCATTTTTTGC TCTTTCCATTTGGTTTCTTCCTCTATCTCCATTTTGGAGGGCTTAAATGACTTCAAAT TTAAAAGTCAACAACAGAGTGCAGCACATTCTATTAGCTTTGCTGTAAATATCTGAT TGGATCGCACC
SEQ ID NO:254	Middle	LPZ-225	GGTGCGATCCGCATTAAGAGAAGCATACAAGAAAAAGAAGTACCTGCCTCTTGATT TGCGTCCCAAGAAGACTCGTGCTATCAGGCGACGCCTTACCAAGCATCAGGCATC ATTGAAGACTGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATG CAGCCAAGGTGTAAAGCACAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTCGCG GGATGATATTGCCTATTATATTTCCGTCCAAGTTTTTGGCAAATTCCTATTTGCATCA GAATTCAAGTTATGATAGGTGTTCTTTCGTTTTTGAGCAGTTGATATTGTTTATCTTT TATTTCTATTATTAATCTTCTAAGTTGGATCGCAC
SEQ ID NO:255	Late	LPZ-226	AAACAGACAAATATAGAAATATGCATACATAAGTCCCTGCAGAATTGTTTTCCGCAA TGAATTCTGGTTTATGGCAACATTACCTACTTAGTACTAACCCTAAGATTATTTTCAG CTCTGATAAGTGGCATACGTGTATCAATCTTGCATGAGTCTATCCCTGTTTTAATCT TTTGTTGGGATCGCACC
SEQ ID NO:256	Late	LPZ-227	GTGGAAGCTTCATTGTAAAACACTACTGGTTTTGAGAGAACAAAATATATACGCTAG CCGAGTGGATTATAACAAAATATAGGCTTTATTCTATTGGATCGCACC
SEQ ID NO:257	Late	LPZ-228	GGTGCGATCCCATACATTAACATAGCCATCACAGCCCCCAGTGGCAAAAGTACCAT AGCTGCAAAAACATTATAAAACTAACATTCCTACAAGGAAATAAAATACAACTAAAAA AGCAAGCAATAGGCATTAGGGGAGGGAGAAGCTAAAACTATTAAGCAACTTACATG GGATGAAAGGCAATTGCGTTTACTGGATAAACAGTATCTCTGCCAGCCTCTGACTT GCGATGACATTTAAAGGCATATTTTTTAAGCTTGACCAGCTTCAGATACATCATAAT ACTCCATAGCCATGCGAGCTTCCACAGAACTAAGGGGCAAAACCTGTTCCATTTGG ATCGCATCA
SEQ ID NO:258	Late	LPZ-231	GGTGCGATCCAACTGAGAAGGGTGTTTGGTGGAAAGATGACACCAAGTGGGTTCT CTATTCTCCAGAGGATGCAAGAAAAATTCTGAGAGCAAAGAAGAATGGGGACTCAA ATATTACGTTGGGTTCTGTTAAATCTGCCAAGTACCCTTCAGGAAAGCTTTATGCCA TAGACCTGGTGGCCATGAAGCAAACCAATGTAAACACTGGCTTCTCCAGAGATATC AAAATCATCAATTCTTGCCCTACTGATGATCAGGAAGATGTAGAGTCTGATGAAGAA GATGAATTATTCACATTCTCTCGTCCTGTCAAAGTTGAAGTGATTAACCAGAGCAGG AAACCTGATAAGATTGTCAAGATGGTTCCTTCTGTCACTGTAGACCTTGAGAAATTG ACTTCTCAATACCTCCTGGAGGATGAGTGCAATTTGGTTCTAAAGCTTCCCAGGGC TGCAGCTGCCCAATCGGATCGCACC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:259	Middle	LPZ-233	GGTGCGATCCAGCTAATCAAACTTAATGGAGAGCCCTTCCCAGGAAGAGTAAATGG TAGTCACTTGAAGCCCTACACGGGTGGGCTGGCGGTCTGACTAACTGACCAAAAC ATAGTCTTCGCGACCCAACAAGCCAGACAGAGGTGTGGGACTATAAGCACAAGTAC TAGAAGCTAGCATCAAAGTAGAGAATTAAGTTAGATACAGATGATTCAGAAGCAGAA ATGGAGCAGATCCAGACCACGGTAGCATGGTGAGTTACGAACCTTCACGCCACAC CAACGCAATTGGTTAAGACTTCGCACTAGGATCGCACC
SEQ ID NO:260	Late	LPZ-234	GGTGCATCCATAGTTCCTTTTGCTAAGCGACTACTCTATCTCTTTTGACATTTCTCC AAATATTGGGTCTTTCAGTTCCTTCAAATGCTAGAATCATATCAACATGGGATTTAG TGAGGCCGCAATACTAACCAGGGCATTAAAATAATACATTTCATTGATCCTATTCCC AAAACATTTCCCGCTATCGTACGTTGACTCAGCATATTTAGAGCAATTCTTCTTACA AACCTTAAGAAGGTTGTTCATGATAGTCTTTCCGTCTGCAATATTGGATCGCACC
SEQ ID NO:261	Late	LPZ-235	GGTGCGATCCCACCCAAGAGTTAAATTCACTTCTCCGCCTTTCTGAGGAAGAGCAC TCTTTGGATGATATGAAAAGTGGTCCACTCTTAAAAACCGTATTCGGAACCCTGTTC CGCGGACGGTCGTATGGCGTAACCGGCGCAGACATTTTATCTCCTCACACAATATC AACATTCAAGTCCCCGCTGTTCCCCGTTGCCTTTCTCTGCTCCCGACCGTTAAACA AGAACGACCACAAGAATGAACAACACCGCAACCGAAACCTGACCCTCCACGTTGTC TTCGGTTCGGATCGCACC
SEQ ID NO:262	Late	LPZ-237	GCGGACGCCTGGCAAAAACAGAGGGTATGCTCAAGCCTTACAGAAATTGAAAAATA AGAGAACGTATGACCATCAATCTCAATCTCAAGAAAAGAAGTTGCAATACGACTCCA ACACTTTTGAAAGTTGGAGGTTTGCTCTTTCTAGCGTTGCAGACATGGTTGGTTTTG AGCTGGAAGCGTGTAACGGGCACTTTACAGTTGCGGGAATTGGAGATTGAGGACC CCCTCTCAAACGTCGATAGGGAGGCTAAGCATCTATAGAGGATTGTGATTGGTCCT TTTCCGCTACATGGAAAGAAAGTCAAACTCAGAAAATTACCAGAAGAATTCTGTCGT CTTCTCGCAGCCGT
SEQ ID NO:263	Late	LPZ-239	GACGTTGTAAAACGACGGCCAGTGTAAAGAGCAGCCCCGATGCGCCGAAGCTCGC GAGGGAAAAGCTGCAGAAGATGGGACCGATGACCAAGAATGAGATCATCATGAGC GGCACGCTACTGGTCACGGTGGGTCTTTGGATATTTGGGGGAATGCTGAACGTGG ATGCTGTTACTGCAGCGATCCTTGGTTTGTCTGTCCTACTCTGCACAGGCGTCCGC
SEQ ID NO:264	Late	LPZ-240	TACGGCTGCGAGAAGACGACAGAAGCAGAACCTGCCAATATAGGATCAATTGAATG TTGTGGGATTGCTGCATGCCCACCTTTCCCAGTTATTACTGCCTTGAAGAACCCAC AGCCAGCGAGTAAGGGCCCGGGTTTCGAACCAATCACAGATGTAGGATAATCGCT TGAAACATGCATAGCGAATATGCCTTCCACATTTTCCAGTGCTCCCTCCTCTATCAT TCTTTTTGATCCTGCACCTGATTCCTCTGCAGGCTGGAAGAGTAATATGACAGTTCC CTGTAACAAATGCTGACGTTGTTGCAAAATCTTTGCACCACCAAGAAGCATGGTAA CATGTGCATCATGTCCACAGGCGTCCGC
SEQ ID NO:265	Middle	LPZ-241	TACGGCTGCGAGAAGACGACAGAAAAGAGGCAAACCGAGCTCGACACCTCCACTC AGAGCATTTGCAAAAATCCACAACAAATCTGGAGCCAAGGTCTTTCCCTCATTGAAA ACATTTATCGGACACATCAATGTCTGTAGTCTTTCCCATGGTCCATCCAGAGTAATC ACGGGAAGAACAATGCACTTCAGTTCAGAATTTTTGATGACAGCTATCAGCTCCTG ATCCTTTGAACCAGGTATATAATAATCTTGACCTGACTCCTGTTTCAACAGTGTAGA GGTTCTGTCAACCTCAAGCAATGAATCGGCAGAACTTCCATTTGCTGTTTTGTCAAT ACAGGCATTGTTTTTACCAAGACTGTGACGCATCTTCTGTCCTTGTCTATACAGTGC AGTTTGTTCAAGCATAGACTTATGTGCTAGAACATGTCTTCCTTTTAAATTGTAAGA GAAATGTAGGGGTTGACTGCTTTTACTGAGGCGTCCGC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:266	Middle	LPZ-242	ACGGCTGCAGAAGACGACAGAACCCTGGCTGACTACAACATTCAAAAGGAGTCTAC CCTGCATCTGGTGCTCCGTCTAAGAGGAGGCATGCAGATTTTTGTTAAAACCCTTA CAGGCAAAACAATTACTCTGGAAGTGGAAAGCTCGGACACTATTGACAATGTAAAA GCTAAGATCCAGGACAAGGAGGGAATCCCACCTGACCAGCAGAGGTTGATCTTTG CCGGAAAGCAGCTAGAAGATGGTCGTACTCTGGCCGATTACAACATTCAGAAGGA GTCGACCCTTCACCTGGTGCTCCGTCTCCGTGGTGGCTTTTAGGTTGGCTGTTGT GTGTCAATGTAGTCTGGTGATGTTCAGTGGTTTTCCTGCTTAATCCTTTTTATGTAT GCATGTGTTTGTTGTGTTTGTGTTTTGTCTCTATGTTTTTTCTACTTGGTTTGTCGGT CGGTTGAAGCCCGGCTGGTGTCCTGGTAGGCGTCCGC
SEQ ID NO:267	Middle	LPZ-243	GCGGACGCCTGGACAAACACAGAAGGCGAAGTAAAAGCCAGTCTTACTTTTCATGT AAATACTATCAAACTGCATGGCCGTTCCGCTGGTTGGCAATACCACACCTGCGCCG GTAGTGCCAATGAACACTGCACCGGCAGCTCTTTCAGAAGTTGCAGAGGACTTACC ATTTTAATTTTCACGGCATCCCGTCAAACGGCGGGATGCTTTTAATTTTTTAATCAA AAAAAATATTAATTATGGCACACAATATTGTTTTCAACGAACAGACAGGCAAACACA GTTTCTTTAGTGTAAAAGAAAAAGCATGGCATGGTTTGGGGCAAATTGTACAGGAC TATCCCAACAGTAAAGAAGCATTGCAATTTGCAGGGCTTGATTTTGAAGTTTGCAAA AGGCCCAATATTCACAGGCTTGATAATGGTAATGAGATTATTTCTACCAGTTCATTC TATACTTACCGTCCTGATACCAACGCCATATTAGGCGTCCGC
SEQ ID NO:268	Late	LPZ-244	GCGGACGCCTGAACATAGGAGCATTCTTAAGCATATCAGGTATAACCATAAACCTG ACTTTGCTGCCCCGAATAAAGACATGCTCCAATTGGGATACTTTTCCATCCTTGGCA GTGTAAGTGATGCCCTCGAGCTGGCAATTCCAGTTATCTTCGCATTCGATCATGCT ACCCCTGTACAGCTCGCCACTTTTGAGTTCAACTGTCACAACATGCCCGGCTGCTT CATGGAGCAACTTCACAGGAATCCCCAAACTTCTGCTCATTTTTTTGTCACTGCTCA AAAACCCTAAACCCCAGATAAAACCCTCGGTTCTGTGCCTTTTATCCCCGGGTGGC TTATTGTTGCAGTAGTTGGCAACGGCTAGACTTACTCACATTTTGATTTCAATCTTT CTAAGTTTGCCCTTTTGGGTTTTCCTCACAGTAGATCCTATTTTATGTATTTTCTCGT CTTCTCGGCAGCCGTA
SEQ ID NO:269	Late	LPZ-246	GCGGACGCCTGCAGGAATCGGCCGATTTGCAGTTCGAGGCATAAGCGCATCGAG GTCGCGTTCGATGTAGCAATTAAGCGCGCATGAACCGCCGCTAAGCAAGCCAGTC CCAATCAAAGCACATGCAAAGCGGATGCAATCAAATCTTCCGTTGTAAGCAAGCAC AAATCCAACTGCACATGAGATCACCACCATGAATGCAATTCGAGTGCGAGCTAAAT CCCAAAACGCTGCGAGTGTCCCCTGAAGGCGATTCGTATGTAATATTTGACCGCTG CTCAACACAAGCAGTACTCCAAACACCAGTGCTTCCGCCGTCAATTCTGTCGTCTT CTCGCAGCCGTA
SEQ ID NO:270	Late	LPZ-247	CTGCGAGAAGACGACAGAACACAGACACAAAATTTGGAAACTACAGAAAAGACCAT GTCATGAAATCTTCATAATTGGGCTTCAGATGCAGAGGGGGTCGGTTTTGGATTAA GCAATGGCTGAAGTGCTTTGACAACAATACTCATGTTAGGACGAAAATCTGCTTCAT ACTGCACACACAATGCCGCAACAGCAGCCATCTTTGCAACAGCCTTTGGAGGATAT TCACTCTTCAACTTGGGATCAACACACTGCTTTACTTTGTCTTCACTCAATCTTGGA GTTGCCCAAGTAACAAGGCTTTGTTGTCCCCTAGGCATTGTATGGTCCACAGGCGT CCGC
SEQ ID NO:271	Late	LPZ-248	TACGGCTGCGAGAAGACGACAGAAAGAGACAGGCTTGGACTTCGTGGCCTTCTTC CACCACGCATTATTTCTTTTCAGCAGCAATGTGATCGTTTCATGGTTTCTTTTAGAT CCCTGGAGCATAACACTCGAGATGGTTCAGCTGACTTAACAGCTCTGGCAAAATGG CGTATTCTTAACAGATTGCATGACAGAAATGAAACACTATACTACAAGGTTCTTATA GATCACATTGAAGAGTTTGCTCCAATAATCTACACTCCAACTGTAGGATTGGTTTGT CAGAATTATGGTGGGCTGTTCAGGCGTCCGC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:272	Early	LPZ-249	GCGGACGCCTCAATAGTTATGGAAGGGCAGCTGCACTACTTCAGCATGAGTGGAG GCCTAAAAGTTTTGTTAATCTTTCTGGTGAGGTGGACACCAAAGCCCTTCACAACA GTGCAAAGGTGGGGCTATCTCTGGTTTTGAAGCCTTGAAGGATATGCACTATTTGG TACAGATTTAAGCGAAGGTCTGTGCCAAATTTTTATTGGAATTTTTGAGTTTTTCCTT TCAGAATAATTATTTCAATGCCTGTGTTTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:273	Late	LPZ-250	GCGGACGCCTTTTGCCCAATTAACATCCCTGCATCTGCGCATTAAAAATTGATTGC AGACCTGAGGTTTAAGTGGAAGCTTCTTCCACCATCTCTCCCCTGTTTAAGGAAGA CCCGAAACCCTAGCCACTGTCTCCTCTGTGACTTAAAATTCCAGTTCACCAACCTTA ACTCTGCGTCCGTTAAAATTCTGGGCAAACTGCACTGCCAATTGGTCATCATATCCT CTGAATTTGGCAAAGAAAACATAGGTCATTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:274	ND	LPZ-251	GCGGACGCCTCGTCAATCCATGGTTGTAAACATGCCTTCAAAACTGTTTCCTTATGT CGCACAATGTCTACATGTTCCTTGAGCGATTTTTCCTGCTGCATTGCGAGCCTCTG TGTAAGTCCCACTATCTGCGCTGTCCCTTTTACTTCATAATACTTCTGTCGTCTTCT CGCAGCCGTA
SEQ ID NO:275	Late	LPZ-255	TACGGCTGCGAGAAGACGACAGAAAAAACTGTATACGAGTAGGCAGCGAGTCCTG GCAGTATGGGAGATTGAACTCCAATTACATTTAGTTACAAGTAGCATCAACAGTGAC TGAGCCAAGAGCTCTACACAGAAAAATAAAATAAAAACTGTATATATTTACAGGAGA AACCCCAATGGCCTCAGGGCCTGAATAAATCAATCGCAGCGGTGGTCGATGTGGC CTTTTCAGGGCTGCAAATCTTGCAAGGGGAAGCCATCATCCTTGTTCCGTATCCTT TTTGAGGGATAGCGAGCCACGCAGCCAAGATTTGAAGCGATTGAATACTTTGGGGT GTCGAGAACGCACCAGAACAATGCCACTCGAGAAATACTACTGTGATTACTGTGAC AAACAATTCCAGGATACTCCCTCCGCTAGAAAGCGACATCTACAAGGCGTCCGC
SEQ ID NO:276	Late	LPZ-256	GCGGACGCCTGTACCGTATTGGAATTCTAAACCCTTCCTTGGTATAGGGTTTTCGC CACCCTTGCGTTCATTTGGTTTTGTATTACGTCCGATTCCTCCGTCTGCGAGCTCTC TGCAACTTGGCAATTTCATTGTGATTTTATCCTATGATGCTTCGTATTTGTTTGAAGC TCGTCCTCCTAGTTCTCTGTGATACCAGTTGGTAGTCTGCAAGTTTCGATGTGGGT TCTTTTAGCTGGTCTGGGGTTTTGTTGCTCTGAGTATGTTGAGCTGCATGCTCGTG GCGGTCTTCACGGCTCCATTTGTTCGGAATCTGTTGTGGAAGTGTCTCGGTCATCT GTGGAACTGTGGAAACCTGGTAAGATTTGTTTATCTGCTTGTGTCTAAACTGTTCTT GAGTTTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:277	Late	LPZ-257	GCGGACGCCTGCTGTTGAAGAAGGATGAAGTCATTGTCTGCGGCCCTGTTCAGCA TGATTTCGGCATTCTTAATCTGGTCAACCAGTCAGAAGGTGGCGCTGAAGGTGACG AAGAGGCAACCTGGGTAGCTGCACTGGAAACTCAAGCTGCAAGGGGCACCGACCC TCAGACTTCGCGCGATTAACTTCTCCCTCTGGCTAAGTCGATGCCAAGGTCCTTGT TCTGGGTTCTTCTCTCTGTTTCGCATGTTGTTCTTCTCTCTGTTTCATTTGTTTTTCT TCTGTCGTCTCTCGC
SEQ ID NO:278	Late	LPZ-258	GCGGACGCCTGCACATACAAAGAACGACAAAAACAAAAGCATAAAATCCAATAGAT GCAACTATATATCAAGTCAGAAATGATATAACTCATCATTATTACAAAGAACAATAAG AGTGGAACCATAATAATAGTCGTCTATTATTGATAAATAAAGAAGAATACAACCATA GTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:279	Late	LPZ-260	GCGGACGCCTGTATAACATGCACCAAGAGACCCAATCAAAGCACATGCAATCTGTA TATATAGCAGAATAACAGCCAGGGATTGCACTCTATCGTAATCGCGAAACCACGCA CTAATATGTGCCCATGCTGATGATGCACACAGCATGTTCTGTCGTCTTCTCGCAGC CGTA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:280	Late	LPZ-261	GCGGACGCCTGAACTGTATAGAGTTGAAACTTGAGGGAAGGCTTGCTGCCACCAA AGCCTCCCTCCTCTTTCCTTGGCGGTTCGTCACCTCCTTTCGCGTCAGAGCCCCAA TTCCCCTCCTGCGCACACCAGCAAACTGCATCGAATGTTTTTTCCACCATTCTGTAA ATTCCCTCGGAGTTACCTTGGGGCAGAAGCCGCATTGAAGAGCATTGAATGCTATT CATTATCCCACCGTAAACTACCATTGCAACCTGCCTGTGTATCGACCCGCTGTCCT CTACGCGTGGCTGGCACATGGCGTCGTTAATTGCATGTTGACACCCGTATCCGGG TGTGCTTGTGTGCTCGTCTGCATATCATGTTTTAGGATCTCATAGAAGGTGGACCA TTCTGTCGTCTTCT
SEQ ID NO:281	Late	LPZ-264	GCGGACGCCTCTTACAATGTCTCTTAAAGATTGGAAAGATTGTCTTGTCTGCAACC ATAACTTCCGCGTGCTTTCTTATTAATGCAACCCACTGTGATCCTTTCCGCCATTTA TCCTTTCGAATGGTTGGAGCCATTTTTGGGTTGTACCGACTAGCTTTTGGGTCTAC AAAGCTGTCTACAAAACTCTTTGGAGATGACATTACATAATCATATGTATAGCTGAA GTTGTACAAAGGTACACAACTATCTGAAACCAAAATGAATCTCTCGTTAGCTGGATC CTCGAGTGCTTTCCTAAGTAGAATACGCTCCGCTTCTATCATACTGGCTTCTCCCCA AAGTACCTGTATGCTATCACTAAGCTGCCAGCCGTAACAAAATGTACATTCTGTCGT CTTCTCGCAGCCGTA
SEQ ID NO:282	E,M	LPZ-265	GCGGACGCCTTGCTAGGAGAGCTCTACGCCATTATTTGAACGATTGAGCCGAAGTT TCACCGTTTAAGGCATTTGTGTCCCAGAGGTTATTGGAGATTAGCAGCTTGGATTT GGCTGCTTCGCTCAGCGCCGTGATTCAGCTTTTGATTGATTCTCTCCAGTTTCATAA CCTGTAACGACAATGGCAATGAAGACCTACACATTTGCAGTGGCAGCTGCGTACGC TGTAGTCCTGATGTTCGCTCTCTTTGGCATCGCAAAGGCTGCTGATGCACCGTCTC CCAGCCCCGTTACTGGCGCGGGTTCCATGGACTTCGTTCCTTCTGTCGTCTTCTCG CAGCCGTA
SEQ ID NO:283	Middle	LPZ-266	GCGGACGCCTTATCAGCTGGGGGCATTCATAGGTATGGAAATTCAGATCAACTTCA GTGGACAGTATGTGGATTTAGGCGACCTGTGACAGTTCACGATATCTATTCATTTCT ATCCAGAGACAGATTCCCATACTCACCTCCGTCCTTCCCATATATTTTCTGGAAGGC ATCATGTCCTCCCAAATTTACTCATTTTGCCTGGCCGTCGTTTTACAA
SEQ ID NO:284	Late	LPZ-268	GCGGACGCCTGTTGCCACAGAAGAATGAATAATGCTTCAAATTTTGAGACCTCTTC GGAGGAAAATCCTTGTTCTTACTGCCTAACCACTCATGATGATCTGCGTCACGCTG ATTATGAGCTGCAATTTAAATTATTTCAGATGAAACATTCCCATATTGAGCTTGCAGA CAAGTTGCAGACCCTTCAATTTCAGTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:285	Middle	LPZ-269	GACGTTGTAAAACGACGGCCAGGATTAAGGTTCATGAGCTCCGCAACAAGAGCAAA TCAG
SEQ ID NO:286	Late	LPZ-270	GCGGACGCCTCTAGGAGCCGGCGGAATTCCTGTGAGCTCGAATTTGCCGAGCAG GTTATTGTCCTTCGTCCGCGCTCGCTCACCTTCATATACTTGAATTAGAACCCCAG GCTGATTATCTGAGTAAGTTGAGAAAATCTGCTCCTTCTTGGTTGGAATGGTGGTG TTCCTCGGTATTAATACTGTCATTACACCTCCCGCTGTCTCCAACCCCAGACTTAAT GGCGTGACATCTAGCAACAGCAGGTCCTGCACCTTCTCGTTGCCTTCGCCGCTGA GAATGGCAGCCTGCACAGCTGCACCATATGCCACGGCTTCGTCTGGGTTAATGCT CTTACAAAGCTCTTTGCCATTGAAGAAATCTTGGAGCAATTGTTGTACTTTGGGGAT ACGAGTCGAACCCCCGACCAAGACGACATCATCTATTTGGCTCTTGTCCATCTTAG CATCTTCGCATACATTTCTCCACAGGCTCCATACTTCTCCTGAAAAGATCCATGTTG AGTTCCTCGAAGCGAGCTCGCGTAATTGTGGCGTAAAAATCAATTCCTTCATATAG AGAATCAATCTCAATCGTTGTCTGTGTAGTAGAAGACAGCGTTCTTTTTGCCCTCTC ACATGCTGTTCTCAGCCTGCGAAGAGCTCTGGCATTCCCGCTGATGTCTTTTCTGT GCTTTCTTTTGAATTCCTGCACAAAGTGATTCACCATTCTGTCGTCTTCTCGCAGCC GTA
SEQ ID NO:287	Late	LPZ-271	TAGCCATCGCCATTTCTATAATCTTAGGATCCTTGCTGAACGATAAGCCCATAAAAT TGATGCACTGCCTCGCTATCCCTGGCCGTCGTTTTACAACGTC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:288	Middle	LPZ-272	GACGTTGTAAAACGACGGCCAGGAAATTACAGCTACCTCTAACTGGTTTGACGGCG TTGCATCTTATGAGCCGCAAGGGTTCGAATCCTCTGCGGGCCAGATCTGCGATGG AACCCTGGGCGAGTGCAATGATGATGAAGAAGAGTTTGCGATGGATTCTGAAGCG CACGGGAGGCTTCTGAGGAGGATCCGTTACTATATCAGCTACGGAGCATTGGCTG CTAATCGCGTTCCTTGCCGACCTCGGTCTGGGAGGTCTTATTACACTCGGAATTGT TACGGCGCAACAGGCCCCGTCAGACCTTACCACAGAAGCTGCACTGCTATCACTC GTTGCAGGCGTCCGC
SEQ ID NO:289	Middle	LPZ-273	GCGGACGCCTGGGAAGCAATGGATGGGTGGCTAGACGCCATCCGTCTTGTGTATA CTATTTTTGCACGCGGAAAGAGTGATGTCCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:290	Late	LPZ-274	GACGTTGTAAAACGACGGCCAGATTCAAAAGAAAAAATCCTCACTTCTTGGCTCCG TTTGCGCTCCCGCCGAAGCTCCTCTGCAACCCCTCTGCAGCGTACACTGCATCCC GCTCGCGGTGCTGGCTCACCTCGCAGGTCCGCTGACGGTAAATGGTTTCCAATAA AGCTATTTGTCCTCTACCCAAAATCCATCTAGCATTCGTTGTGGATTGACATTCTGC CATTTCTCTGCTTTTCTGGTTGATATGCAAAGATTGAAAGCCCAATTGCAAGCAGTG GTCGTGGATTCACTATAAGGCGTCCGC
SEQ ID NO:291	Late	LPZ-275	GACGTTGTAAAACGACGGCCAGGAATAAAACAAAGCATCACTGCAAAATTTCAAAC GTGGTAATAACGGCTAGCCAGCTCGACGTGAAGGCAGTGGGGGCCTTGAGGTTGC CTTTTGGCGTTCAAAATTGGCTAGACTACCATAACATAAATATTGATTTCTCAGTGA CATCACTGGTTTGGAGTCATCCACAGCCTGTGCACCAGTACGGCAATTGCCTTTTA CATGAAGCCATCCTTTCACTTTTACTTTTGAGATTCTCAGAACTGAGGGGCTAGGC GTCCGC
SEQ ID NO:292	Middle	LPZ-276	GACGTTGTAAAACGACGGCCAGCACCTTCCTAGTCCCCTGTTCCATTCTCCTGAAA TAGGAGCAGTTTGACCCAGTCCAGTTTTCAGAATTGAGAATATGAAACAAAGAACCT AAGCATATGAGAGAACATACAAAGACTTTGTATAAACTACTTTTCACAGGATCTCAA CAGCCCTCTGCTGAGATCCATTTGATACAAGGCCCCTTGCATCTCCACCCTCTCCC TTATCACCTCCACTAGAAAGATGATGGAAAGCAGACACATGGAAATGTTGCTGCAG GCGTCCGC
SEQ ID NO:293	Middle	LPZ-277	GACGTTGTAAAACGACGGCCAGTTAGGTTGTATATTGATTGATGACTCTTTGACTCC ATTTATGAAAACATCTTTGTTCTCGAGATTTAATCAGTATTAAGCTTTCAGAGTGAAG TTCAGTTTGATCTGCATAAACCTGATCCACCATATCTACATCACATCTAAAATTACTA AAATGTGAGGAGATGGAATTTGTTTCTTGAGAATCCCTATTCCTCATCGACACTGTT TACTGGATCAGATCCAATCAAACTCTTGAGAAGTAATCTCTGGAAAGAAATTAAAAA GTCTTTACCTGAATTATCTCGATATCAGAAGCAGAAATTATGATACATAGACTTCTTA ATAATGAAGAGTCATTTTGCCAACGTTGTCTTTGCCACCCCACCAATCCCCATGATC CCAAAGATCTGAGGTTTCCATCTCTATGTGGCTGTGATAACACTGGATTTTTCAAAA ATCTTCTACTTTCGCATCCAAACCTTTTTGGGATATTT
SEQ ID NO:294	Late	LPZ-278	GACGTTGTAAAACGACGGCCAGGGGGATGGGAGATACAGAAAGATTCCGGATAAA AGGGAGCAATGAACGGCTGGTTAAAGCGTAGTCCACCACACTAGCCCCACCTCCA TGAGGCCTACACGTGAAGAAGCAGGATTCTGGGAAGCGCGAGAGGCCGTTCAAGA TTATCAGCTCATGTGATTCGCCCAACTGCAAAAGATGTCTACCGTAGGCTGTGATG GGGCCCAAGGCGTCCGC
SEQ ID NO:295	Late	LPZ-279	GCGGACGCCTATCAGATGGGTGAGTTGACCGACATTTATCGTCCGATAAATGTTTG AGGCTGATGTCATGGCAATCCACGTGTCTGCACCATATTTCATCGGAGCCCCTCGT CGGAATATTCCATCGCCGGAGAGCTGGCGCGATAGGTTTCAGGCGGCCGGTTTCT GGTTTGCAGCTGTGGCTTCCCGCGCGCCTTAACTGTTGGCCCGCGCGCACAGGG GAAATTACAAATTTCAACATATCCAATACCATCATATAACCCAACAACACTAGCAACA GATCCTGTTCTGTGCCATCGTCCAACTCTTGA

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:296	Late	LPZ-280	GCGGACGCCTTAATTCGACTACAAAGATACTGAAGCCAATGATGACAGGTTGTGCC ACTTTCCCAGCTGATAAAGACAGCTCTGAAATTGATAGAGCCAGAACTCCAGCTGC AATGCTCCCCAGAGCCTGGTTGAAGCGCTTGCTAAAGGTGGCACTTTATAGACCGA CCCAAAACCTCCCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:297	Early	LPZ-281	GCGGACGCCTACTGGAAACCCGGTCCACCGAAGGCTGAAATTGTCCTGCTTTGTA TACCGAATGGCAGGAAGGTTGTCGAGCATCAGGTTCACCTGGTAAAGATTATCGAT CCTATGCTTCAATACCTTCAGCTGCTCTGCCCCAAGGACAGTAGTATTGCACAGGT AAATTTCAGATTCATTGACATTCATCCGGAAGCGATATGGTGAGTTCTCGATCCTGT CCCCCATGAGGAGCTCCCCAAGATTTTCTGCCATGTCCTTCACACCATCCAAGGGC TTGCAGAAGGGCAGGCTGTAATAGCTGTAGGGAAGCTCTGTCTCGACTGAGGTAA GGGAATTGACGTTCACCCATAAATCTGACCCCTGGGAGAATATGATGTGAGGAATA CAGTGCCCAGTAAATATAACTCCGCATTATACGTTTGTGTGTGCCTTCCCCAATATT GCCCCAACATAATCAAAACCCACAATCCCAAATCCTGGACCGTCGTTTTTACAACTG TC
SEQ ID NO:298	Early	LPZ-282	GCGGACGCCTTGTCAGGACCAAATGTGTAAGAAACACCTCTGTCATTCGAGCCCCA TCCTTGAATTGCATTGCAGGGGTCTGACCAAAGAAGATCACATAACAACCCTGTAT CTGGCACATCTGTAGGTCGAGGTATATTCTTTATTTGTTCCAAATTGGTCAGTTCAG GCGAAAGACCACCATGCATGCATAGGATCTTTTCATCTATAAGTGCAGCAACAGGC AGGCAGTTGAAACAGTCTGTAAAAAGTTTCCATAGTCTTACATTGAATCTGCGCTTG CACTCATCATAGAAACCATATATGCGATTTATTGAGGCACATTCATGATTTCCCCTC AGAAGGAAAAAGTTCTCTGGGTATTTAATTTTGTAAGCAAGGAGGAGGCATATTGT CTCTAGGCTTTGTTTGCCCCGGTCCACATAATCTCCCAAGAAATAAGTAATTTGATT CTGGTGGGAAGCCACCATATTCAAAAAGCCTTAGACAGATCAGAATACCGGCCTGT CGTTTTACAACGTC
SEQ ID NO:299	Early	LPZ-283	GACGTTGTAAAACGACGGCCAGGAGACGGGAATACCTATTTTTGGGAGGATTATTG GGCTCGGGAATCAGCATATTGATGTGGCTGCAACTCGCATCCTCGATCTTTGGTGG TTCTTCGGCGATTTACACATTTGAGATCTACTTCGGTCTGCTAGTTTTCCTTGGGTA TATTATATTTGACACACAGATGATCATCGAGAAAGCGGACCATGGAGACTATGATTA TTTAAAACATTCACTGGACCTCTTTATTGACTTCGTTGCTGTATTTGTTCGCCTGAT GGTCATAATGGCAAAGAATGCAGACAGTAAATCCAGGGAAGGGAAAAAGAAGAGA AGGGCTTGAACTATGTGAGATACAAAAATATCGAGAATAGAAGGGCTTGAACTAGG GCTTGAAAGCGTCCGC
SEQ ID NO:300	Middle	LPZ-284	GCGGACGCCTATCAGACAAGGGTTGTTGACCGAACTTTATCCTCTGAAAAGTGCTT GAAGCTGATGTCATGGCAATCCACGTGTCTGCACCATATTTCATCGGAGCCCCTCA CACGGAAACAACCTTAAGCCAAAAGGTGGTGCGATGACTTACCGGCCGTTTATGGT TTGCTTCGGTGGTTTTCTGTTGGGTGGTTTCCCGCGCGCGTTAACTGCTGGCCGT CGTTTTACAACGTC
SEQ ID NO:301	Late	LPZ-286	GACGTTGTAAAACGACGGCCAAGAGGGGGAAACTCCCAAAACACTTTTCCATTTTT CTTCTTTTATTAAACTTCAAAGTATTTTCCAACAGAGTTACAAGGGGCCAACCATGT CCAAATCCATGCATTTACCAAGTACAAAGAATGGTAGTCCTTGGCTTGACCTATCGC ACTAGCCAAAAGTGCCAAGTCCACAACTAGGGTGTGCCCAACCTAAGGTTGACACC TTGCCTAGAAAAAACCCCAAACTTGGCACCACAAATAACACAGAAACACAACTCTTG ACCTCTGCCAGAAACCAGGCTCTCTTGGGAAAGCCACACCTCTCTCTGTGATATGT CTTATCTCCAATTTCCCTTTTTGTGATGCACTCCCTTGCTTGTGGTTCTGCGATATC ACACAAACTTACATTTCTGCGATTTTTGTTTCTTGCTTCTCCAAATCATGCGATCTTA TTTTTAACCCTTGAGACCCTTCACACTTTCCATCCATGACGTCACTTCATCGTTTTA GCCAATTCGTCATTTGGGCATGTTGGGCGTTGGGTCTACCCGTATTCCGGTCGTAC AGGCCAAATTGACCATTTTGGTCCAGGTGGGTGCACCCATTCCTGGAGGGCGTTC GGC

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:302	Late	LPZ-287	GCGGACGCCTCCACAGAGCTCACACATACAATATACTATGATGCCTCCAGAACTAT GGCACTCTGTATGCCGCTTCAATATGGATTAGCCCACACTGCGCCATCCAATTAGG CGAATCAACCTTATAGCACCATCCACAACCTCCAGCGCTCTCTTTTTCACGCTAGAT TGGCCAACTACAGGCTTTACAACACTACTCATATACAACTCAACTCGGCTCCTCTGC TCACCACTAAATCACACAGGCTCCAATCGCTAGACAGAGCCACTACACAGGCACTA ATAGCCACTACACAGGCACTAATCTTGGCGTCCTCCACCAGGTTCCAACAACAACC CCAAATTGCATATGCACTCCACAGTGAGCACCAACTAGGTCCACACAATAGGCCAC ACCAACAACACTCCAAGGACCCTAGATCCTGCCTCACCCAGACACCACTAGGCCTT CCTCACAGCTCACCTAAGTGAGCCAACAACTGGCTGGGCACACAGCTCCCAACTAT ATGAGCACACAGCCCAACTACAGCTCCACCACACGCACAGCTACACGCACAATGC CTTCTCAAGTTCACAGCCACACCATAACGCAGCACAGTTCTTACAAACATATCTCTC CAGGCGTCCGC
SEQ ID NO:303	Middle	LPZ-288	GACGTTGTAAAACGACGGCCAGGATAATGGACACGAGAAACCTTTGGATGTGCCT CTAAAGTGCGGGCAATCCTTAAAGCTGTTGAATTTTGTTGCTGTACACGAAGGTGC AGGGTCTTTATGCCACGAAGAATCAAGTACGCTGCATTTGGACTTAATACACCTCC CAAGACATTGTGCAAAGCACGTACTGTGCCAATAACCTTGTTTGAACCACTCAAACT GCCTGCAAGAACATCATTATGACCTGCAATATATTTAGTTACCGAATGCAATACAAT ATCTGCGCCGAGTGCTAACGCTTTCTGGTTAACAGGCGTCCGC
SEQ ID NO:304	Middle	LPZ-289	GACGTTGTAAAACGACGGCCAGTCATTATTGACAATAATCCTTTCAGCTTTTTACTG CAACCTTTAAACGGTATACCTTGCGTTTCTTTCACTGGAGCACACTCAGATGATAAT CAGCTTTTACAGGTGCTCTTACCTCTGTTGAAGCATCTTGCCACTCAGGAGGACGT GCGCCCTGTGTTGTATGAAAGATTTTACATGCCCGCATGGTTTGAAAAGCGTGGCA TTCCAGCATCTGAGTGGCCCTTGTGACTTGGTTTTGATTTTGGATACTCTTTGTCAT TTTGGGTCAAGGTAAAGGTGTACGTATCCAAGTGATGCAAGCGTCCGC
SEQ ID NO:305	Middle	LPZ-290	GCGGACGCCTGATAGCACGAGTCTTCTTGGGACGCAAATCAAGAGGCAGGTACTT CTTTTTCTTGTATGCTTCTCTTAATGCGGATCGCTGGCTCTGAGAAATCACAGTCAG AACCTGAGCTATTGATAGCCTCACGACCTTGATTTTAGAGAGTTTGTTGGGCGCTC CTCCAGTGACCTTTGCAACTCTGAGCAAGGCAAGCTCAGCCTTGAGCTCCTTGACC TGGCTTAACAGCTCGGATTTGCCCTTGTGGCGGACTCAAGGACCTTTAACCTGGG CGTTCGT
SEQ ID NO:306	Late	LPZ-293	GCGGACGCCTGGTGTCGCTGGGCCAGTTCAAGTATTTTAGCAACAGTGTTCACACT TATTCCCTGTGATATTCTTGACTCACACAACCACCTTAACTGACGCAGACCATATCG ATCTGCTGCTGTAAGCAAATGTTCGATCATTGTCTCAGGTGTCAAAAAGCAAGGGG ATGGATCAGAAAGCTCTTCTAAATCTGCATGCTCCTCTAAATCTGGAAGGGTATCTT TGTAAATAAAGTGTAACATAGCCTTAAACACCTCTGGCCGTCGTT
SEQ ID NO:307	Late	LPZ-294	GACGTTGTAAAACGACGGCCAGAGGTGTTTAAGGCTATGTTACACTTTATTTACAAA GATACCCTTCCAGATTTAAAGGAGCATGCAAATTTAAGAAAAACTTTCCTGATTCAA CCCCCTGCCTTTTGGCACCCTGAAGATGGTTCAACAATTTGCTAACGGAACCAATT CAAAAGGGCCGCCTCCATTTAAGGTGTTGTGTTAGTCCAGAATATCACAAGGAATA AGTGTTAACACCGGTGCCAAAATACCTGAACTGGACCAACGACACCAAGCGTTCGC C
SEQ ID NO:308	Middle	LPZ-295	GCGGACGCCTTGTAATCCAGGGCCTTGAATATTGTAAGAGAAGATCGAGAAATAAT AGTTTTCTTATTATCAGGAATCACAGCTTGAAGAAGGCAGACCATGGACTCCCACT GGCTTCGTGATATTGAGTCCCCAACAAACATTAGTCGTTTTCCCCTCAATCTCCACA GCAAGTCTCTGGCATTGAATCTGCGAAAGGAACACCCGAGTGGCTTCCACCTCCAT TTCTCGTAATCAGAATCTGGCCGTCGTTTAACAA

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TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:309	Late	LPZ-297	GACGTTGTAAAACGACGGCCAGCAGAAGACCAGTGCAGTATGCTGCAGCATAGTT TGTAAGCCCTACTTCGAGTCCATAACGAGGCAACTCCCTAGAATAAGCAGCCGACA TAACAACATCTCCCGCAAGAGTTGCATAAATGATCTGTGCCACCACATCCTTGTTGC TGAATCTAACGACCAATCGGTATTTGGGTGTGTTGTACTTGTTCTTATCTTGGTTAA TCAGGCGTCCGC
SEQ ID NO:310	Late	LPZ-299	GACGTTGTAAAACGACGGCCAGCATCCATTGCAGAAATTTTGGGGGCTATATTTAG CAACAGATATCACAGCTGTAAGTTCAAAGTTGGACCCTTCTTCTTCGACATCTTTTC CAGCTGTGCAATAAACTGAACACTGTCCTTTTGGATAAGCTTCCTCAACATATTTAG AAAGTTCAACATCCAAGACATTGCGGTACTCCTCAACATATATGGATGCAAGTTCAT CATCTGCAGCTGGTCTCACCGCTGTACAAACTTGTTTAACATGGTTGACAGTTGCA ACTTGAGCAGTCCGTGGATCCAAATAATGAGTTCCGTCAAGCTCACTGAACTCAGT CACAATCACCTGGCCACTTTGATTGGGCATCTCGAGGGATATCATGTGAGACTTGT TGTGGATGGGGAAAGCGTCCGC
SEQ ID NO:311	Early	LPZ-300	GCGGACGCCTGCATAAACATCGCTACCCTGGGGATGATTAATAATAGTACCAGGGT TAGGATTTTCTTCATCTTGAGCGATATCATCATACATAAAGACCACAATGTTTTCCTC TTTCAAACCGCCTTTCCTCAGAATTTGGTAGGCATGGCAGATATCAGCCTGATGCC TGTAGTTCCAATAACCGGAAGAACCAGCCAACAGAATAGCCCACTGAGTACCGATC GTATCACTATCATCAACGATATGATCGGTGGGCATTTTCAGTACTGAATCCCAACCC CTTCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:312	Middle	LPZ-301	GCGGACGCCTAGACTGGGCATACCAACTACCTTCCTCATGCCAGGCCATGGGCCA CCTACCTGGTACTTAGGCATAACACCTTACTTACGAGCATGCCAGGCTCAGTCAGA TAGGCATGCATCCCACCCACCTAGCTATGACCCAATCCTTATAAACACTAGATATTC TCCCTGGCCGTCGTT
SEQ ID NO:313	Late	LPZ-303	GCGGACGCCTAGACAATCATTAACTGAAGATCTGTAAGCCATGACAAGACGAATAA AACGAAGCACGGCGCAACCAGCGTGAATATTGACGCCTTAATTTCATTCAACTGGG TTGCGGATTCTTTATTCCTCAACAAGTGTTCGATAGCTTCACATACGCAAGGCCCCT TTTACTCTCACCTTCATGGTTTAATGCTGTAACCGTCGAAGGTTGATGAAAGGACTT GGATGATGATGTTGCCAAAAAAAAAAAAA
SEQ ID NO:314	Middle	LPZ-304	GCGGACGCCTGCTCAACACCTGTTATAGTCATTTCTTGTTTCCTTTTCTCAATTTTC TCTTTCGAATGACCGCATTGAAATTCAGGCTGCCCAACGCGTTTTTGTTTTCACAAT TAATTTTTGAATCATACGCGAAGATCATGATGAGAATGGTTGTGGAAAAAAACTGTT TGTAAATATTTAG
SEQ ID NO:315	Middle	LPZ-306	ATATCACATTACCATTCAAAAAATAAACATTTTACAAAATACAATTCCATAACAATTTT CTTCCCTGTTCCAACCTCCACAAAAGTAAATGATCGTATAAGAAATTAACTACCAAC AAAAATCCCAAAGTTAAAGGAAGACATCCCCAAAAAAGATGTAACTTTCAAAACCGG ATGACTTCACTCCTGCCATTGCACCTAGTCATTTACTTCTCAGAGGAGTTTGGCCCT TTCTTCTTTCCAAAAGTAACCACTGCGGTAACAAACCGGCGGTTGTATTGCATTCG CTTGTAGGCGCGGCCTCTAGGCTTCTTCTTCTGTCTTGTTTGGCCACCTTAGGGTC CGC
SEQ ID NO:316	Middle	LPZ-307	GCGGACGCCTTGGTACAATGGACTTGCAAAAATAAAATGAGTTCTCATTTGTGGGT GAGATGCGGATATTTTATGCATAGGCACTTCATGGAGATGTGGTTTATAAACGCCA TCTTAATATCTGTACCTATTACTTTCAAAATATGAAGGCAAGATGGAAAGCTACTCAT CTGTTGTGAAGTCAGAATGTTGGTAGCGGTTGGGCTCTGAAAGTAAGAAACTTTTT GATTGGTTTAATTAAATGAGGGAATTTGCCTGGTTTCCCTCTTCCTTCCGAAAAAAA AAAAAAAAA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:317	Late	LPZ-308	GACGTTGTAAAACGACGGCCAGACAATATTGGAAGGGAGAAAGGCGCCAGCAGGG TTGAGGGGAAGAAATGCATAATGACATATATAATGAGATCTATTTGTATACGATATT ACGGGTACGATCGATGATTCGAGCTACGATCCCATACGACGCTAAAGCGTAATTAC ATATATAATAGATGCATTTCAGAATGACTTATCTATTTCATTACGCGATATTATATAC GTAATTACGTATATAATTGCAGAGATCTCACCGACCAACCAAATAGTCTTTCATTTC ATCCCAGGCGTCCGC
SEQ ID NO:318	Late	LPZ-309	GCGGACGCCTGTATCACTAGAGGTGAATACTCAGCAAGCAAAACTGAAGGATATTA TTGAAAAAGCTGTCAAGGCTAAATTGGGTGTCAATTCCCCATTGATCATGCATGGTT CTACACTTTTGTTTGAGTCCGGTGATGACATTGAGGAAGATGTTGCTGCACATTAT GCACAAAACTTAGAGAAGACGTTAGCAGAATTTCCAGTTCCAATCACAAATGGTGTT ATTCTTACAGTAGAGGACTACCAGCAAGAGTTCTTATGCAGTATTAATATTAAGCAC AGAGATGACTTTGATGAGGAGTCAGGTGGCATTGTACTGTCTGGAGGCGTCCGC
SEQ ID NO:319	Late	LPZ-310	GCGGACGCCTCCTTGTAGATACCATACATGAGTCTAAGATCAAAATCATACAAGAA GAGCTTCATTCCGGGCCTCACCTTTTCTACAAGCTCCTTTTTGGCTGGTGGAAAGC CAAACACTCTGTATCGGAAACACTCCTGCCTAGTTTCAGAATTACACATAAAAATCA AGCCGGCAAACCTATCTTTGCCACTGCCATCTTCATTGTTTGCGTCCTGGCCGTCG TTTTACAACGTC
SEQ ID NO:320	Late	LPZ-311	GCGGACGCCTTACTAAAACGACGGCCAGATGTGTAATGGGGAAAATGTGTCATGAT AGTTGGGTACAAATAACGAGCCACCTGCTCTATGTTTTCGAAGTTTTCTGTTGGATT TGTCCGGGTGAGAGAGCGTTCGTTCGTTGCGCGAGAGGGGCAAAATGCTGAGCG TGGGGAATTGCCATTGCCGCCCCTGGAAGTGCCGCACGAACGCGATCACATTTAA ATCACCATTTACTTCATCATCACCATGGTTAAATGCAGTCCCTGCTCCTTCAAACAG GAACTTCAGATCCTTCAAGCTCGAAATCTCCGCCTCTGCTTCCTCGAAGACAAGAC TCTGTGAGGAGGAAGCGCAGCAGCTGAGCTTAGCGGATCTGCTGAAGCCCGGTG GCCTCGCCCCCGATGGGTTCTCGTACAAGGAGAACTTTACCATACGCTGCTATGAA GTCCGAGTTAAACCGCACTGCCACCATTGAGGCGTCCGC
SEQ ID NO:321	Middle	LPZ-312	GACGTTGTAAAACGACGGCCAGCAACCAAATAAACCCCACATGTGCTCAATGTTTT AGTATAAAAGGAGATGACTTAAGAGTCATTTCACACACACTTCTATCTTGATTTCTCT CCACTTGTCTTGGGTTTTAGTGGAAGAGAAATCTAGGAGTGGAAGCCCTAGACGTT GGAGGATAAGAAGGCAACCCTAGAAGGCAGAGCTAACGCTATCCTAAGGCAACCC TAACGCTATCCTAAGGCGTCCGC
SEQ ID NO:322	Late	LPZ-314	GCGGACGCCTGCTCAGCACCTGTTATAGTCATTTCTTTTTTCCTTTTTCTCATTTTTC TCTTTCGAATGACCGCAATGAAATTCAGGCTGCCCAACGCGTTTTTGTTTTCACAAT TAATTTTTGAATCATACGCGAAGATCATGATGAGAATGGTTGTGGAAAAAAACTGTT TGTAAATATTTAGGTGACCAACAATTTTCATGATTGCAATCTAAAGTTGATAATTGAT TTATCGGGTCGACATTTGTAATTATTAACACGGAAAATCTGAGGCTTACAATTTTTG GATTGTAAATATTTAGGTGACGAACAATTTTCATGATTGCAATCTAAAGTTGACAATT GAGTTATCGTGTCGACATTTGTAATTATTAACACACAAAATCTATGAGGCGTCCGC
SEQ ID NO:323	Late	LPZ-315	GCGGACGCCTCATCAATCCATGGTTGTACACGCGCCTTCAAAGCGGCTTCCTTATG TCGCGCAGCGTCTACTTGTTCCTTGAGCGCTTTTCCCTGCTACATCCGCGCGAGCC TCTGTGCAAGGGCCACTGTCTGCGCGGTCCCTTTAACTTCGTCGTACTTCTGCTGC AGCTCACGTGTCTCTATTTCTAAGTGCTATATATTTGGGTCCTCCTGCATAGTAGTG AACTTCGAACGACTCCTCAAATAGCCAGGTGTAGTCTTTCATTGCACTATTGATCTC CACTATTCCTGCTATAATGGCGCTAACATGCTGTTCCTTCACCTTTGGCGGAGTTG AAGGCTGCGCCTTCTTGGAGCTCGGTTATTTGAAGCTGAACCTTGGGCATATCTTC CTTCACCTCGTGCATCCCCTGCTTCGAGTTTCTGGATGCACGCCTCCACTGGGTCT TCTGCTGGGATGGGCAACTCTAAGACCAACTGGTATGCGTCGC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:324	Middle	LPZ-318	GCGGACGCCTTCTTCAATCCATCAGGCCTGATTAATGTATTGACCTTCTTTGTCTGA ATGTCATACATTTTTTTCACTGCATCCTTGATCTTCTTCTTGTCTTGCTTTCTATCCT TTCTCTTGCTTTCTATCCTTTCTCTGGC
SEQ ID NO:325	Late	LPZ-320	GACGTTGTAAAACGACGGCCAGCAAAATTGATATAAAGAATAGACACATCGACTCA AATGAAGTGACTCAACAGTTCATTAATTCATGTCAGCTTGAATGCATGGACATACAC CCATAAATAGGCAGTTGGGGTCACCCAAAAGAACATAGAAACATCTCGCATCTCTC TGAAGAAACTCGGATGGGTACAGGTCTGTGACTTCGCATATTTTGAAGGAGCACTC TCTTGGATAAGTACAATATAGGTACCATCTCGGACTCGCCTGAAATCTCGCAAAGA AGTCTCATTCTCCTCCTTGTTACAGGCGTCCGC
SEQ ID NO:326	Late	LPZ-321	GACGTTGTAAAACGACGGCCAGAAGCATCAATAAACAAAATGACAGATTAACAAGT TCTCTCTTAATCTTAAGAGAATACATCAACATCCAAGTAAAGTCATAACACATTTACA AAATGGTGCCACGGTATCCATTCTCTGTAACAAGGTTTTTCTGAAAATAGTTTTCCT CTTATCTATGTAACTCTTCATAGGGATGCCTGTGTCAACGTGCCATATTCCCAAATT TGGCCACAATCAAACCTTCCTCATTAGAAGAAACAATCTCTGGTCTAGCTCAAAATT GGCAAAATTTCCAGCATCTCCCTTTAACATCATTAGAAGGCGTCCGC
SEQ ID NO:327	Early	LPS-097	GGGAGATGCTAATTTGAAGCCCTTCTCTGAAGGTGGACAATTCCAGCAGCAGTGGT CTAAAGCCCCAATATGGCTATAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGG GTCGGAGAGGACGAAGCTGTGGATCGCTCTTACCATCTGTGCGGAAGGTGGTAGC AGAATTCATTGGAACGTTCTTCCTCATATTTGTAGGATGCGGATCTGTCGTTGTTGA TAAGATAAGCAACGGTTCCATAACTCATCTTGGTGTGTCGCTTGTATGGGGAATGG CGGCCATGATTGTAATTTATTCCATAGGCCATATTTCTGGAGCTCATTTGAATCCTG CAGTGACGTTGGCCCTTGCGGCTGTGAAGAGATTTCCATGGGTTCAGGTTCCAGG CTACATAGTAGCTCAAGTATTTGGATCGATATCTGCTGGGTTTCTCCTACGTTTCAT GTTTGGAGAAGTGGCATTCATGGGAGCCACAGTTCCTTCAGGCTCAGAAATGCAGT CTTTCGCTTTGGAAATTATTACTACGTCATTGTTGGTGTTTGTGGTTTCTGCAGTCG CCACTGATACAAAAGCGGTGGGTGAATTGGGAGGTTCAGCAATTGGAGCGACCAT CGCAATGAATGTAGCCATATCCGGACCAATCTCAGGAGCTTCAATGAATCCAGCAA GGACAATAGGATCCGCAGTGGCTGGCAACAAATATACAAGCATTTGGGTTTACATG GTTGGGCCTGTAATCGGTGCGCTAATGGGTGCAATGAGTTATAACATGATTAGAGA GACAAAAATGTCCGAAAGGGAGATTATGAAGAGTGGGTCATTTGTTAAGGACATGG GCTCCAGCGAATCAACAGCATAACAACTTAGAGATTTNTTGCATTCCCGAGACGGT ATCCAGTGATAGTGGAGAGTAGTCATAATAAGATTTGTGAAAATGTTTGTGTAGATT AATGTGTAAAATTCAATCCATCAACCATGAAGCGAACTGCATTCCGTTTTTAAATGT TTATTGGATTTGAATTAATAAACAGCTTATACGTGAAAATCCCTACTTTATGTACGGA
SEQ ID NO:328	Early	LPS-098	ACTATAGGGCACGCGTGGTCGACGGCCCGAGCTGGTATCCGATGAAGCTAGATTC AATGGTTCAAGTCCTATGAAAGCTAGATTGGAGAATTGCAAAGAAATCTAATCTCCG TTAGTTGTCCCAACCACTGACTCGCACCCAATCAGAGTATATTAAAGTTAAAGATTA TATAAAGGTAAATTGAACATTTATAAAATCTTAAATGTATTTTTAGAGTTAAACATTAT ATAGAATATTTAATGTAGTATAGATATAATAAAATATTAAAAATTAATTTCTCTTTACT ATCAAGTGAATAAAAATAAAAAATAAATGTAAGACAATATAATAAAAGACTTGTTTTT AGTGCATTTTTTGGACTCTTCGTTATTGTGTGGTATTGTGTTATTTAAACTGATCTTT TTACTGTATATATGGATGGGTTACCCATCAAACTTGTGATTTCAATAAATTCCTCCC GGATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAAC TCACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCA TCTTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTT ACATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTT CAAACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGGGGGGATTCTCACG GCTTAACATTCATGGANCCGATTACCTTNCTANCCAACCAAGGGTTTTAACCTGGAA CAAATNCCAAACCAATTACCAGCTTNACAAATCAACCGAGCCGCCCNACCGGGATC ATTTTGGTCAAGTCTCGAAAACNGGCATTGGGTATATGGNATATGGAATTGGAATT GGATCAATGGTAACCTTGGGANAAGCTTAANTTGGAAANCCCTTTTTTTTGANGGG GGCCAANTTCCCGNNCCCCCGG

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:329	Early	LPS-099	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCTATGGTCGACCTGCAGG CGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTCT CCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGGC TTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCAT CTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGACT GACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTCA GTTAAAGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCCT CACAGCAAAAGATGCGTTGGAGCTCGTTGATTCTTTAGTTTGAACGGTCATACCTTT ATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAATTTAGG TGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTATC TAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTAAAA TTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGGGAGGAATTTATTGAA ATCACAAGTTTGATGGGTAACCCATCCATATATACAGTAAAAAGATCAGTTTACCAG CCCGGGCCGTCGACCACGCGTGCCCTATAGTAATCGAATTCCCGCGGCCGCCATG GCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGTCGTATTAC AATTCACTGGCCGCGTTTACACGTCGTGACTGGGAAACCCTGCGTTACCACTTAAT CGCTTGAGCACATCCCCTTTTCCAGTGNGTAAAACGAAAAGGCCCCNCCATCGCCT TTCAAAAATTGGCAACTGAANGGGAAGGACCCCCT
SEQ ID NO:330	Early	LPS-100	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAG GCGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCC CTCCGACCCTCTTCCATAGGTATAAAACCCAGAATTTGGTGAGCAGGAAGAATTTC CATAGCCATATTGAGGCTTTACACCACTGCTGCTCGAATTGTCCACCTTCAGAGAA GGGCTTCAAATTAGCATCTCCAAGTTACATGGATCTATTCTATTCATATATTTATAAC AATGCTGCTTCGAGACTGACAAAATTATTTGTTGGCGCTTGTTCATCGTTAGCTGTA ATGGTTTGGATTGTTCAGTGTAGGACCAGCCCGGGCCGTCGACCACGCGTGCCCT ATAGTAATCGAATTCCCGCGGCCGCCATGGCGGCCGGGAGCATGCGACGTCGGG CCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGT CGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCC TTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAG TTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCGCGG CGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGC CCGCTCCTTTCGCTTTCTTCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTC AAGCTCTAAATCGGGGGCTTCCTTTAGGGTTCCGATTTAATGCTTTACGGCACCCT CGACCCCAAAAAAACTTGATTAGGGGTGATGGGTCACGTAGTGGGCCATCGCCCT TGATAGACGGTTTTTCGCCCTTTGACGNTGGAAGTCCACGTTTNTTTAATAGNGGG ACTCTTGGTTCAAAATGGGACAACACTTCAAACCTTTTTTGGGGNTATTTTTTTTGAT TTATNAAGGGATTTTTGCCGNNTTTNGGGCCTTTTGG
SEQ ID NO:331	Early	LPS-101	ACTATAGGGCACGCGTGGTCGACGGCCCCGGCTGGTTTCAATAAATTCCTCCCGG ATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAAATTTTAGACCATAAAAACTC ACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCATC TTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTTAC ATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTTCA AACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGAGGATTCTCACGGCTA ACATTCATGACCGATTACCTCCTACCAACAAGGCTTTAACTGAACAATCCAAACAAT TACAGCTAACAATCAACGAGCGCCAACGGATCATTTTGTCAGTCTCGAAGCAGCAT TGTTATATGTATATGAATAGAATAGATCAATGTAACTTGGAGATGCTAATTTGAAGC CCTTCTCTGAAGGTGGACAATTCCAGCACCAGTGGTCTAAAGCCTCAATATGGCTA TAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGGGTCGGAGAGGACGAAGCTG TGGATGCTCTTACCATCT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:332	Early	LPS-102	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAG GCGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTC TCCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGG CTTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCA TCTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGAC TGACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTC AGTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCC TCACAGCAAAAGATGCGTCGGAGCTCGTTGATTCTTTAGTTTGAACGGTCATACCT TTATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAATTTA GGTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTT ATCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTA AAATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGGGAGGAATTTATT GAAATCACAAGTTTGATGGGTAACCCATCCATATATACAGTAAAAAGATCAGTTTAA ATAACACAATACCACACAATAACGAAGAGTCCAAAAAATGCACTAAAAACAAGTCTT TTATTATATTGGCTTACATTTATTTTTTACTTTTATTCACTTGGATAGTAAAAGAGAAA TTAATTTTTAATATTTTATTATATCTATACTACATTAAATATTCTATATAATGTTAACTC TAAAAAACATTTAAGATTTATATATGGTCAATTACCCTTATATAATCTTTAACTTTAAA TCCCTGATGGGGGCCAATAANGGTNGGGAAACTAACGGAAN
SEQ ID NO:333	Early	LPS-103	ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTTTCAATAAATTCCTCCCGG ATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAACTC ACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCATC TTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTTAC ATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTTCA AACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGAGGATTCTCACGGCTA ACATTCATGACCGATTACCTCCTACCAACAAGGCTTTAACTGAACAATCCAAACAAT TACAGCTAACAATCAACGGGCGCCAACGGATCATTTTGTCAGCCTCGAAGCAGCAT TGTTATATGTATATGAATAGAATAGATCAATGTAACTTGGAGATGCTAATTTGAAGC CCTTCTCTGAAGGTGGACAATTCCAGCACCAGTGGTCTAAAGCCTCAATATGGCTA TAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGGGTCGGAGAGGACGAAGCTG TGGATCGCTCTTACCATCT
SEQ ID NO:334	Early	LPS-104	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCTATGGTCGACCTGCAGG CGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTCT CCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGGC TTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCAT CTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGACT GACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTCA GTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCCT CACAGCAAAAGATGCGTTGGAGCTCGTTGACTCTTTAGTTTGAACGGTCATACCTT TATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAGTTTAG GTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTTA TCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTAA AATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGAGAGGAATTTATTG AAACCAGCCCGGGCCGTCGACCACGCGTGCCCTATAGTAATCGAATTCCCGCGGC CGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGT CGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGCG TACCCACTTAATCGCCTTGGAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA AGAGGCCCGGACCCGATCGGCCCTTTCCAACAAATTGCGCAACCCTGAATNGGGA AATGGGCCCCCCCCTNTTACCGGNGCAATTAAACCCCGGGGGGGNGNGGGGGTT CCCCCCCCCGTGGACCT

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TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPS001	0	249.4	1400.9	827.6	1683.8	2019.4	189.2	4303.9
LPS003	701.2	555.9	2815.2	2445.1	3249.9	3094.7	227.1	3111.6
LPS004	466.1	335.5	2652	2701	2644	2329.6	218.5	2332.4
LPS006	753.1	332.7	3287.3	2964.5	2832.2	2688.9	182.1	1591.9
LPS007	685.2	226	2010.2	1911.3	2600.4	1730.1	181.5	2737.7
LPS008	652.8	274.8	2415	2219.3	2607.1	2294.9	155.7	1292.1
LPS010	558.3	356.1	2667.6	2881.1	2584.3	1573.4	161.7	1041
LPS011	3536.1	424.7	4021.5	3793.8	3590	3182	160.5	1471.7
LPS012	809	408.4	2206.7	2187.1	2282.2	2422.5	462.4	1483.2
LPS013	1211.1	391.6	2294.7	2652.6	2005.4	2167.8	166.8	1570.5
LPS014	2191.9	432.5	2651.8	3013.5	3341.2	3586.7	178.8	3527.1
LPS015	1197.9	306	5651.4	14828.6	20242.8	21558.2	1427.2	34472.3
LPS019	1830.2	334.5	3329	3954.4	4347.5	4658.2	312.1	4743.1
LPS020	675.2	327.8	2258.3	2284.7	2542.7	2321.4	171.9	1609.8
LPS023	451.3	337.5	1401.9	1106.8	1766.2	1842.6	109.6	1365.2
LPS024	4585.8	444.5	3006.3	3431.1	3548.8	3759	157.3	4062.3
LPS025	5102.3	397.1	4322.9	4699.6	5067	4973.2	262.4	5240.4
LPS026	1568.7	285.9	1809.9	1830.4	2829.9	2381.7	164.9	1404.9
LPS027	5499.9	458.4	4853.9	5218.6	2598.4	1756.6	457.9	2375.3
LPS028	4812.9	314.9	2368.8	2616.5	3113.3	3292.4	557	4146
LPS029	4464.6	251.2	2334.4	2058.1	2930.3	3219.3	472	3814.4
LPS030	1142.2	352.5	2519.8	2460.9	2499.8	2634.5	378.3	2147.8
LPS031	1067.7	481.6	3510.8	2799.2	3568.2	3257.2	287.9	2209.7
LPS032	1120.2	332.3	3153.1	3032.4	1769.2	1816.7	146.6	2689.9
LPS036	1498.2	1072.9	4633.6	5524.2	5465.1	6350.7	918	14058.5
LPS037	1890.3	320.9	3719.1	3618.9	4138	4518.1	513.4	5087.5
LPS038	2899.5	310.3	4530	4226.1	4491.6	3969	268.4	4245.3
LPS040	527.4	238.1	1433.4	1611.2	1984.5	1506.5	143.9	1988.7
LPS041	506.1	265.5	1958.9	2843.2	2065.3	2016.2	147.4	2781.7
LPS042	1432.1	1140.3	4379	4973.3	4525.4	4340.8	319.6	3009.8
LPS043	696.9	776.2	3933.1	4894.3	3512.2	3664.7	340.6	3098.4
LPS044	57.8	275.1	3365	4261.2	4773.5	4979.9	974.4	10645.5
LPS045	536.1	211.1	1559.5	1415	1498.5	1584.8	562.1	1912.3
LPS046	796.3	231.7	1023.9	306.4	1417.8	1328.2	83.8	946.4
LPS047	5029.9	518.2	3632.5	4262.1	4755.5	4087.9	386.3	4933.8
LPS050	6333.5	2620.8	5271.4	5242.1	5586.4	5560.1	980.1	11444
LPS051	1378	224.4	2328.8	2221.8	2260.5	2715.1	123.7	3670.4
LPS052	1526.4	267.5	2046	1856.2	2186.5	2416.3	99.3	2010.1
LPS053	4438.3	361.6	4087.6	3959.9	4786.5	3666.8	379.6	4256.7
LPS054	1992.9	269.9	2734.2	2388.1	3143.8	2337.7	177.6	2803.9
LPS055	4587.8	334.4	3488.6	3474	4018.3	3101.6	196.2	4309.4
LPS056	5960.7	1333.7	5338.8	5670.3	5674.4	5533.5	446.4	5593
LPS057	2219.9	301.9	2397.3	2356.1	2218.1	2085.6	184.4	2657.8
LPS058	4070.4	299.9	3485.4	3721.3	4113.8	4142.2	239.8	4945.6
LPS059	8729.3	279.2	3885.7	3636	2720.4	3346.7	165.7	3734
LPS060	4580.2	323.7	3027.8	4713.4	4929.1	5047.5	161	4704.8
LPS061	2831.9	366.8	2392	2327.7	2546.5	1991.8	177.9	3036.7
LPS062	1674.1	353	2711.2	2526.1	1847	1830.3	124.5	3584.2
LPS063	5514.4	419.8	5238.9	5020.3	5417.4	5041	250.1	4812.6
LPS064	7417	3166	5229.5	7497.4	7933.1	10261	1088.3	16829.6

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TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPS065	5634.9	343.5	5527.8	5099.4	7833.4	5356.6	237.5	4696.7
LPS066	1015.9	244.5	1702.6	1650.5	2895.1	2437.2	128	2514.1
LPS067	2796.8	240.4	3931.5	4810.3	5407.8	5418.3	202.5	9403.8
LPS069	533.4	189.9	1635.8	1816.4	2114.2	1646.8	119.8	3208.8
LPS070	2516.9	240.6	1909.5	2519.6	2156.7	1777.4	186.4	4362.1
LPS071	592.8	196.4	1789.2	2189.2	1981.1	1304.5	127.6	3430
LPS072	444.2	217.6	1422.9	1509	2065.3	2289.9	122.7	2678.8
LPS073	4362.8	273.1	3094.9	3348.1	3771.8	4075.3	137.7	4259.6
LPS074	32072.9	6816.3	33531	25258.9	38176.4	32687.7	14607.1	37529.6
LPS075	7013.9	472.7	4759.7	4933.9	5452.2	5408.7	409.4	5397.1
LPS076	4236.1	362.6	3131.9	2882	3368.5	3354.6	119.5	3141.9
LPS077	2958.7	276.6	4380.4	4862.5	4475.1	4958.7	218.9	4426
LPS078	23685.3	2642.5	35458.6	25869.6	42378.9	33047.1	25402.2	37189.8
LPS079	4794.3	547.8	4628.6	4821.8	5257.2	5277	829.5	5449.7
LPS080	30454	10527	33713.7	23785.4	32590.9	32210.7	16224.4	37659.2
LPS081	30405.9	28677	35358.3	25873	22338.1	31715.3	36436.4	36650.5
LPS083	5040.1	460.8	3251.7	3487.3	2688.9	2565.9	190.5	2979.7
LPS084	2031	298.9	2843.7	2718.4	2352.2	2165.5	164.9	3398
LPS086	3571.7	320.1	2715.8	2648	1989	2528.4	143.9	2969.7
LPS087	3302.3	337.4	4873.1	5695.8	5407.2	5450.6	670.8	18404.9
LPS088	826.8	302.1	2389.2	2871.1	3180.8	2635.2	138.6	3141.5
LPS089	796.4	321.2	1987.7	2640.6	3299.1	2285.1	143.7	3176.6
LPS090	4031	235.9	3867.3	4064.4	4503.3	4798.4	341.7	4697.7
LPS091	2423.3	196.5	2836.8	3101.3	4049.1	4172	295.2	4612.2
LPS092	2914.9	208.5	4005.3	3138.4	3911.6	4036.1	270.4	4842.9
LPS093	793	195.5	1619.2	1331.6	1909.3	1843	147.1	2772
LPS094	1374	221	2205.5	2028.5	2240.9	2632.2	163.3	2849.1
LPS095	728.7	174.1	2022.6	2112.1	2335.8	1264.6	117.5	2957
LPS096	393.3	168.5	1531.9	1393.4	1893.3	869.1	118.3	1691.1
LPZ001	2008.6	185.4	2535.9	2937.9	3472	1981.8	118.9	2421.7
LPZ002	3529.3	384.6	4579.3	4474.6	3236.7	3855.8	313.8	3237.5
LPZ003	4076.8	275.4	2651.2	2966.7	2829.2	4177.4	378.5	4369.7
LPZ004	5595	687.4	5468.2	5615.9	5243.6	5699.6	601.6	5889.9
LPZ005	5680.5	3353	34994.7	26121.9	42555.1	33144.5	16193.7	37798.2
LPZ006	1199.8	299.4	3013.7	3099.8	3517.3	3397.1	140.6	3370.8
LPZ007	1159.1	462.2	3292.7	2992.5	3121.4	2936.7	235.5	3238.6
LPZ008	1874.3	237.7	3110.8	3236.7	2516.5	3182.2	325.3	4330.1
LPZ009	3331.1	296.3	2348.5	3414	2478.2	3309.5	348	5658.1
LPZ010	3216.3	1186.8	4977.3	5024.7	4564.4	4992.4	442.6	4454.5
LPZ011	4613.4	910.9	4510.7	4515.7	3729	4357.3	371.4	4695.9
LPZ012	1531.5	469.5	2915.3	2611.1	2012.3	3481.4	270.3	3804.3
LPZ013	3495.1	268.8	2125.9	2584.7	3194.7	3787.4	125.1	4929.6
LPZ015	2040	257.6	1971.1	2966.7	2191.1	3056.7	227.1	4156.6
LPZ016	5307	2761.1	8451.7	17219.7	22792.7	15567.3	1073.6	35074.1
LPZ017	2476.4	354.3	3175.5	4330.8	4496.2	4061	273.2	5328.9
LPZ018	3929.4	417.5	12420.2	14916.1	18116	17637.5	2541.6	31981
LPZ019	5404.2	427.3	32190.3	24710.4	42102.7	32342.6	19528	36969.5
LPZ020	576.9	142.9	1451.4	1505.4	3534.8	2679.8	210.9	3046.2
LPZ022	1408.2	155.2	2406.7	2845.7	3042.5	3074.8	189.9	3829.2
LPZ023	562.1	152.8	2096.7	1710	2045.5	2078.9	200.8	2874.3

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPZ024	496.7	158.1	1681.3	1264.7	2102.9	1857.1	132.1	1818.4
LPZ025	5431.3	464.1	13492.2	9726.2	11911.5	13462.8	1262.5	11780.6
LPZ026	1663.2	139.7	2464.8	2760.1	3113	2219.4	159.1	3183.5
LPZ028	5029	190.7	5367.2	5339.8	5483.9	5205.5	482.3	5565.9
LPZ029	961.3	119.2	1805.4	1989.6	2298.5	1998.4	126	2576.9
LPZ030	1457.4	177	2444.7	2687.5	1966.4	1857.2	178.5	3312.8
LPZ031	3092.8	361.7	3564	3925.3	4627.8	5171.4	506.7	5920.5
LPZ032	1906.5	156.8	5542.3	24342	42917.8	33386.1	30058	37998.6
LPZ033	12934.5	354.7	5280.1	7301.2	5638.9	9238.7	375.4	15843.5
LPZ034	1307.4	177.5	1737	2208.4	3213.1	1984.1	150.2	3228.3
LPZ035	556.5	201.9	880.2	1280.1	1654.5	915.1	74.1	1422.1
LPZ037	1356.8	269.7	2072	3110.5	2912.8	2488.2	211	4119.3
LPZ038	4027.9	426.9	5639.9	5872.3	5476.8	5614.6	796.8	5583.3
LPZ039	5059.1	550.6	3807.9	4393.8	3825.6	3889.8	342.2	5164.2
LPZ040	1226.1	236.5	1566.4	1889	1679.1	2263.6	140.6	3331.1
LPZ041	944.2	219.3	1629	543.1	1148.2	1416	90.2	2524.6
LPZ042	570.6	206.1	1129.5	806.5	1448.8	1423.1	75.1	2013.8
LPZ043	1190.2	236.7	1878.8	1024.4	2834.6	2767.4	241.7	3236.2
LPZ045	5315.3	465.7	4933.2	5580.2	5151.1	5205.1	557.3	10754.3
LPZ047	859.5	285.2	1606.2	2099.3	2059.4	1992.6	68.3	3054.8
LPZ049	3232.7	108	1278.6	2834.2	3657.8	3944	244.2	5459.6
LPZ051	3048.1	146.9	2373.2	2067.3	2745	2383.2	179.1	2837.6
LPZ053	2580.3	135.6	2625.8	2088.7	2468.5	2297.2	156.8	3001.4
LPZ054	1838.1	159.5	2657.8	2759.7	2658.1	2224.7	170.4	3444.2
LPZ055	2181.8	151.1	2381.2	2262.7	3228.3	2983.9	139.3	2673.9
LPZ056	4028.3	219.5	2884.6	3416.6	3779.6	3789.9	208	4518
LPZ057	1470	121	1676.5	1629.6	1702.7	1703	112.2	2272.1
LPZ058	1923.3	122.5	2453.5	2169	3127.3	2465.4	160.6	3319.6
LPZ059	1760.4	113.8	2180.6	1832.4	1997.2	1530.8	174.4	3366.6
LPZ060	3296.4	139.3	2571.1	2250.2	2721	2976.9	221.3	3898.5
LPZ061	2495.6	182.8	2663.9	2235	3265.9	4227.1	498.1	4915.1
LPZ062	1992.7	194.9	3296.7	3975.8	3861.5	5642.6	497.6	5606.2
LPZ063	2167.1	145.9	2733	1843.9	3066.6	4961	305.6	4773.2
LPZ065	5641.2	251.7	13690.3	9269.2	8562.8	13254	986.3	9554
LPZ066	6307.3	652.4	12630.8	6968.4	4918.9	5062.2	400.7	5456.8
LPZ067	10838	1548.1	16986	11776.8	5633.2	7054	1014	15262.2
LPZ069	1481.9	209.6	2239.8	1480.9	2496.7	2542.4	250.5	3717.2
LPZ070	1932.5	263.8	1895.1	2221	1555.9	1570.4	145.5	3471.3
LPZ071	3672.6	378.6	4185.5	3050.5	4166.8	4246.2	553.7	5333.4
LPZ072	744.5	210	1210	676.7	1420.2	1393.4	95.8	1997.1
LPZ073	1997.9	235.9	2275.1	2141.7	2613.2	1989.9	170	3489.4
LPZ074	1375.9	237.4	1899.1	1787.3	2472.9	1623.7	125.6	2435
LPZ075	831.4	247.9	1536.4	1773.1	1886.9	920	80.6	1053.5
LPZ076	345.7	251.8	854.8	564.6	1747.1	526.2	55.9	1058.3
LPZ077	2466.3	102.2	949.4	820.9	3093.9	3179.6	202.9	3314.8
LPZ078	3102.1	197.1	3654.2	3261	4204.3	4433.6	400.8	5559
LPZ079	1584.4	108.3	2389.2	2243.3	2624.8	2677.1	208.3	3675.6
LPZ080	12206.5	2043.1	25021.4	8579.5	11707.8	8717.6	1172	18663.9
LPZ081	1368.7	103.6	1902.8	1349.9	2166.1	1597.7	103.5	2709.6
LPZ082	2601.3	140.3	3264.3	2853.9	2799.6	1742.3	251.1	4288.2

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPZ083	1311.9	76.7	1622.4	1071.1	1733.9	1878	104	2007.7
LPZ084	9974.7	801.3	14255.3	8399.1	5763.9	8852.9	542.2	5714.3
LPZ085	4609.8	158.4	3923.3	3729.7	4082.8	3867.3	219.3	4075.1
LPZ086	10874.1	987.4	19189.5	8284.6	5646	9109.8	1116.4	14988
LPZ089	3505.8	211.6	4010	3430.6	3762.1	3770.8	224.3	5341.2
LPZ090	5780.9	581.8	13217.4	6303.4	4694.8	4779.9	425.2	5408.9
LPZ091	5316.1	148.4	2263.4	2139.8	2382.2	4067.2	256.8	14732.6
LPZ092	5448.7	209.4	3631.6	4152.7	2934.1	3403.7	174.9	4943.6
LPZ093	1169	159.4	2097.9	1187.4	2050.8	2350.7	109.4	2605
LPZ094	1245.5	139.7	1547.5	1650.5	1875.2	2009.9	80.2	2376.9
LPZ095	711.2	177.9	900.9	1253.3	1013.8	1395.3	48	1586.1
LPZ096	2122.2	249.7	2929.3	3271.3	2132.9	2224	232.8	4443.8
LPZ099	4306.4	211.2	2603.1	2144.4	3479.2	3488.5	138.1	4085
LPZ100	3373.5	297	3941.3	3149.6	3790.4	3857.5	443.8	5028.1
LPZ101	3007.7	272.4	3546.9	2291.3	4299	3232.1	306.1	4819.6
LPZ102	2092.7	324.7	3167.5	2109.3	3524.3	2829.4	279	4297.4
LPZ103	3602.1	285.7	2923.3	3112.9	2812.9	1318.3	87.9	1739
LPZ106	1359.7	305.1	2680.3	2391.6	2838.5	2097	173.7	3009.6
LPZ107	28560.8	4989.5	20821.7	17880.4	39173.1	27035.1	11973.3	36123.4
LPZ108	4136.8	179.4	4259.8	4978.2	5553.2	4862	837.2	5597.5
LPZ109	3708.3	202.4	3842	3510.4	4638.4	4453.7	469.5	5107.4
LPZ110	4557.2	291.4	5020.6	4801	4487.4	4481.1	552.3	5484.2
LPZ111	1625.6	130.9	2242.1	1982.7	2740.6	2455.4	164.6	3722.3
LPZ112	2887.4	195.8	3813.2	3759.4	3984.8	4167.1	409.7	5461.8
LPZ114	5029.5	213.4	5016.7	4678.8	5036.9	5168.1	302.1	4316
LPZ115	24434.4	2637.1	27958	23684.2	41104.3	30920.9	2153.9	36902.6
LPZ116	8682.9	235.7	5647.3	5316.6	5805.6	9313.7	466.6	16018.9
LPZ117	30879	4843.7	36277.1	24358	24673.1	20545.7	4669.9	5652.6
LPZ118	4023.6	171.1	3743.5	4568.2	3845.4	3783.9	254.3	4782.5
LPZ119	2580.4	114.1	2507.2	3114.1	2544.6	1963.6	127.6	3195.4
LPZ120	1998.8	157	1987.2	1503.1	2331.8	1805.1	131.5	3522.3
LPZ122	2041.4	119.6	2145.6	2430.9	1998.6	2171.8	101.3	2677
LPZ124	2795.6	185.4	2980.4	2672.5	2495.2	3459.4	173.1	3081.5
LPZ126	2559.7	181.8	2560.1	2349.8	3500.6	2362.1	224.9	3646.9
LPZ127	1993.5	169.1	3161	3180.8	3382.5	3321.3	180.6	4058.4
LPZ128	2866.7	263.2	3556.8	3597.4	3545.7	3813.8	306.7	4071.3
LPZ131	1993.5	171.7	1983.9	2069.6	2565	2607.2	80.3	2527.8
LPZ133	2446.7	290.4	3218.6	2847.2	3830.1	2889.5	245	4252.4
LPZ136	1952.3	281.1	2956.9	1870.6	3167.6	2680.6	215.9	4291.6
LPZ137	2833.8	281.9	3264.4	2350.2	3874.4	3532.8	420.8	4935.3
LPZ138	2932.9	1791	5211.5	4502.1	5409.9	4832.8	543.1	4741.3
LPZ140	2284.7	337.4	3680.2	2810.9	3196.1	3191.2	271	4613.6
LPZ141	4726.2	368.5	4792.5	4412.5	5368.1	5466.3	722.1	4956.4
LPZ143	25290.6	2692.2	35967.9	25679.9	43668.3	32612.1	25456.9	36344.4
LPZ144	2620.9	286.6	3948.7	3394.6	4505.7	4142.8	488.7	4776.7
LPZ145	3472.5	171	3949	3194.2	3430.5	3539.9	327.9	4487.2
LPZ146	2612.8	127.3	2482.4	2080	3000.8	2979.1	135.1	3391.3
LPZ147	2447	106.3	2855.1	2237.7	3134.2	2841.8	261.6	4388.1
LPZ148	2036.8	77.7	2559	1932.3	4296.1	4699	359.6	3982.3
LPZ149	5720.7	267.4	5377.3	5408.2	10999.7	5717.7	1078.9	13033.2

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPZ150	5861.7	772	35541.7	26314.8	44633	33238	13126	37853.6
LPZ151	5550.3	3499.3	9012.8	8380.4	11968.1	5716.5	715.8	5536.9
LPZ152	4746.6	352.8	5169.3	5647.7	5384	5394.2	408.5	5382.1
LPZ153	21881.2	2773.2	14738.2	15979.5	16996.8	15756.8	2388.5	30812.9
LPZ154	4869.8	265.9	3244.3	3497	3948.6	3703.3	303.8	4119.1
LPZ155	3904.2	1596.3	5078.5	5482	4631.7	5314.1	553.4	4112.9
LPZ157	4726.5	1732.8	5427.1	5369.5	5213.3	5705.9	756.4	5462.2
LPZ158	15297.4	3817.1	17993.9	17405.3	25168.8	22056.6	2337.4	22375.3
LPZ162	5725.8	4204.8	10380.1	11364	17948.2	14250.8	1934.6	10535.5
LPZ165	5615.2	666.7	5274.6	5486.6	5560.3	5310.9	637.1	5405.9
LPZ166	5889.1	2603	9503.5	10943.7	13743.3	14080.4	1772.5	5772.8
LPZ167	5347.2	1948	5708.9	6769.6	5742.3	5347.9	370	5279.7
LPZ169	3043.8	267.4	1976.6	2851	3451	2451.2	189.8	3420
LPZ170	3507.3	301.5	3532.3	3391.4	4481.4	3398.7	130.2	5604.2
LPZ171	3762.3	780.7	4554.8	4311.7	4936.4	4511.3	398.6	5030.5
LPZ172	5098.2	947.4	5550	6287.9	5135.4	5323.9	1242.5	8539
LPZ173	22580.5	3313.9	35486.9	24974.9	42874	31828.8	26531.8	36066.9
LPZ174	4115.7	221	5241.5	4262.4	5765.8	5554.9	872.5	4815.2
LPZ175	4388.3	1360.6	5563.7	5504.9	5165.3	5182.9	583.2	4602.3
LPZ177	1371.6	94.5	2119.4	2218.6	2730.7	2431.7	143.2	2893.2
LPZ179	3643	195.1	4409.9	4898	5458.3	5319.8	797.9	5677.7
LPZ181	5573.3	215.9	4799.6	5272.2	5825.3	5554.4	1573.5	13689.7
LPZ182	4118.9	107.6	3491.5	3182.1	4617.5	4543.6	478.1	5527.8
LPZ186	5792.2	325.5	4965.1	5182.6	12373.6	11191.4	1804.9	37336.4
LPZ189	33820.3	5188.5	30941.4	24955	43453.2	33115.2	17929.3	38055.6
LPZ194	2807	151.1	2915.9	2955.1	3306.8	3120.2	142.9	4101.6
LPZ195	5345.7	532.7	5597	5628.7	5540.4	5491	545.7	5756.7
LPZ196	4805.1	3512.9	5183.2	6968.6	5465.4	5052.4	786.4	5694.5
LPZ197	7268.6	159.8	5398.9	5673.5	13582.6	15111.9	3499.6	34684.8
LPZ198	7208.3	210.6	5800.8	8043	5439.2	5183.6	409.3	5042.7
LPZ199	3058.3	186.1	2749.6	2667	3713.6	3704.3	243.4	3917
LPZ201	7175.3	236.7	4827.6	5029.9	5523.4	5802.2	1981.9	14614.5
LPZ202	3603.3	1113.9	35531.5	26035.1	44762.8	33837.3	63521.8	38225.4
LPZ203	4325.4	424.4	5517	5387.3	9934.8	5662.1	2104.8	9370.7
LPZ204	32355.9	34690	36443.6	26004.3	44546.1	33680.5	55702.6	37890.3
LPZ205	4904.1	519.6	5162.4	5398.7	5427.6	5325.6	281.4	5770.2
LPZ206	3504.4	319.8	3124.8	4561.7	4192.2	3899.9	255.7	5489.9
LPZ207	32035	24978.7	34825	23371.8	42639.9	32686.4	30672.2	37674.8
LPZ208	25174.6	3118.6	14244.4	13906.3	16694.7	21111.9	2190.1	34542.4
LPZ210	3885.1	422.3	3895.8	4551.5	4205.7	5108.7	258.6	5514.3
LPZ211	2569	176.7	3689.2	2943.5	4001.9	3860.9	250.2	3113.1
LPZ212	5988.8	1244.3	32684.4	11154.1	19853.4	13654	618.3	10736
LPZ213	3406.9	106.8	3964.1	3876.6	4236.4	4294.4	274.2	4874.6
LPZ214	1668.3	55.3	2136.3	2394.8	2390	2269.3	105.8	3436.2
LPZ215	5019.8	139.3	5020.1	5024.8	11013.9	13747.1	1991.7	36930.6
LPZ216	3336.8	1085.4	35895.6	26245.3	44980.1	33834.4	64482.7	38238.1
LPZ217	23512.1	26363.3	36065.8	24685.4	43193.4	31422.4	21462.1	35990.6
LPZ219	4011	256.9	3193.5	3326.3	4509.5	5258.5	455.2	5841.9
LPZ220	8696.5	2383.3	5064.7	5171.3	4923.7	5340	951.7	17530.6
LPZ221	1221.4	83.1	1201.8	707.6	1556.5	2083.9	182.1	3948.8

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FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPZ222	1885	146.1	2834.7	2253.2	2557.7	3382	196.7	4225.1
LPZ223	1048.5	121.2	2339.6	2642.1	2663.8	3573.5	383.5	4579.2
LPZ224	3190.6	118.8	3049.8	2833.2	4373.8	5139.9	858.6	5285.7
LPZ225	25428.2	4079.7	35724.5	25423.6	43300.5	32574.8	38888.3	37219.9
LPZ226	1044.9	130.4	1776.9	1210.8	2757.7	3388.5	326.6	3520.3
LPZ227	1078.3	133	1461.7	973.5	7032.1	9452.8	2043.5	4705.3
LPZ228	3961.6	213.5	3373	4050.7	5575.6	10714.4	2428.6	5928.9
LPZ231	3475.2	230	4096.3	3841.1	5009.3	5690.3	959.9	5514.3
LPZ233	2404	218.2	2170.9	1531.4	4362.7	4198.1	673.7	3350.1
LPZ234	1688.3	312.3	1887.6	1486.5	4228.6	4715.6	724.8	3170.1
LPZ235	2661.6	199.9	2422.2	1852.6	3078.9	2886.6	98.2	3143.5
LPZ237	3174.5	324.2	3032.5	2988.2	3931.1	4587.9	314.4	4588.3
LPZ239	4061.3	309.3	3175.1	2932.1	4131.7	3892.6	122.3	5083.5
LPZ240	3799	316	3730.6	3314.6	3379.8	3538.8	212.4	4784.5
LPZ241	2559.2	62.1	2610.4	1794.5	4165.6	3754.4	134.8	2915.1
LPZ242	29360.5	3262.9	35254.6	25196.9	43028.8	31468.2	7308.4	36768.4
LPZ243	3405.3	88.8	3015.7	2683.4	3678.7	2990.6	121	4001.4
LPZ244	4856.9	483.6	4842.2	5235.3	5317.6	5432.1	205.4	5712.9
LPZ246	1274.8	65.9	2301.7	1922.8	4332.2	4628.8	672.1	4232.4
LPZ247	3894	69.8	2522.8	3389.9	4451.4	4937.1	939.3	5522.8
LPZ248	3016.7	268.6	2883.2	3805.2	3791.7	3777.6	487.1	4585.6
LPZ249	5224.1	138.3	3524.5	4091.2	3022.4	3393.2	149.9	4101
LPZ250	1060.6	46.5	1400.9	1246.9	1419.5	1411.2	118.8	2908.4
LPZ251	1336.8	248.5	1354.6	1049.3	657.6	924.3	70.3	2064
LPZ255	3787.8	171.8	4801.8	5076.3	4608.1	4965	340	5636.6
LPZ256	536.6	61.6	865.5	971.6	1130.8	1327.7	82.7	936.9
LPZ257	844.5	112.6	1507.4	1537.8	2337.9	2745.8	341.5	1610.7
LPZ258	2588.5	142.3	3443.1	2902.2	4576	4976.4	1182.9	3619.6
LPZ260	897.7	113.7	1677.9	944.3	1217.6	1286.6	170	2928.2
LPZ261	981.3	132.1	1499.6	743.4	1590.8	1953	67.2	1652.1
LPZ264	4559.3	231.3	4348.5	2856.3	4869.2	5179.7	412.3	4698.3
LPZ265	21063	2793.9	26928.5	12365.5	13816.5	12134.4	691.6	17954.8
LPZ266	1642.4	130	1767.5	1463	1633.8	1410.5	59.4	1444.5
LPZ268	2451	114.2	2803.3	2495.4	3126.5	3433.7	79	4261.3
LPZ269	15670.7	3660.5	35782.4	21720	40375.2	31597.3	2024	35213.6
LPZ270	3541.2	240.8	3803	3132.4	4827.8	5213.6	79.9	5473
LPZ271	5590.7	677.2	5465.4	5197.1	5703.4	5615.2	309.2	5732.7
LPZ272	27369.6	3445.9	35824.6	22832.6	40684.8	27398.4	1732.9	37016
LPZ273	1107.3	46.1	456.7	336.3	1879.3	1654.1	65.4	971.9
LPZ274	3936.2	114.5	3192.3	3024.1	4983.3	4907	293.9	4933.5
LPZ275	2567.2	42.9	1760.4	2091.8	3656.5	3800.5	77	2585.4
LPZ276	560.9	32.9	1075.4	1878.9	1889.9	1766.2	66.8	1294
LPZ277	423.7	34.6	1199.1	1169.8	1376.8	1383.9	91.9	1123.7
LPZ278	323	39.7	937	382.9	770.1	935.2	66	1403.4
LPZ279	965.9	70.7	1907.5	1368.2	1783.7	1603.9	133.2	2438.8
LPZ280	390.7	19.6	175.4	42.3	464.9	631.5	29.9	2074.9
LPZ281	84.3	8.2	0	0	0	0	9.7	0
LPZ282	1849.7	28.4	315.1	34.2	664.3	1097.3	21.5	1229.5
LPZ283	10678.6	329.2	5134.7	5311.1	4772.3	8591.1	226	9633.6
LPZ284	996.1	39.8	236	147.2	2349.5	981.1	26	719.7

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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPZ286	563.8	77.1	1031.1	945.9	1347.4	1601	81.2	1303.6
LPZ287	1045.7	123	2057	1475	1730.9	3003.6	149.9	2493.5
LPZ288	1201.7	116.2	1797	1448.8	1648.3	670.4	80.6	3700.4
LPZ289	1922.3	113.3	2515.4	3395.3	3460.7	3369.4	70.8	2183.8
LPZ290	14629.5	3945.8	34659	24047.3	40474.8	27786.2	1348.2	27566.4
LPZ293	4364.8	385.4	4664.2	3170.9	4321.6	4789.8	74.6	5095.8
LPZ294	564.7	171.4	1257.5	705.2	1357.7	1610.2	18.6	2027.6
LPZ295	823.1	97.3	2102.7	1056.2	2899.7	2698.3	39.4	2448.2
LPZ297	5273.4	169.1	5229	5074.4	5727.8	11512.9	423.2	10966.8
LPZ299	1564	161.1	1743.9	1752.3	2764.1	2660.5	63.5	2791.9
LPZ300	3068.3	205.4	2406.8	1881.8	2898.6	2758.4	0.2	2007.2
LPZ301	1979.7	233.1	3207.1	2109.3	4343.5	3713.8	40.4	2690.6
LPZ303	509	32.7	281.3	877.7	893.1	751.5	30.1	1373.8
LPZ304	2531.1	289.3	3809.4	3406.7	3674.8	3517.4	158	2652.7
LPZ306	22632.7	2861.2	34933.8	25435.6	40453.9	30906.9	1505.9	34032.8
LPZ307	2604.4	1395.2	4780.6	6945.3	4419.2	4416.9	232.6	4299.8
LPZ308	1093.9	60.5	2028.1	1751.6	1770.8	1891.9	92.4	3245.8
LPZ309	286.1	26	480.4	378.4	589.6	731.4	38.4	1062.4
LPZ310	2284.1	129.5	1622.7	1091.7	1207.1	3089.4	101.2	3624.9
LPZ311	3309.9	43.6	2782.6	2956.3	2828.8	4446.7	95.8	5593.4
LPZ312	446.3	52.7	1577.7	1221.4	542.2	518	56.1	1952.6
LPZ314	378.6	26.9	333.9	355.8	682.2	701.2	61.7	732
LPZ315	3897.5	115.2	2611.9	3145.8	4296	5240.2	151.3	4499.3
LPZ318	9709.6	767.1	19964.9	15678.3	20611.8	19600.2	475	18079.9
LPZ320	1126.7	82.8	1215	1002.7	1502.5	1555.3	67.5	2964.4
LPZ321	2944.7	85.4	2590.7	2597.6	2550.3	2962.7	72.1	5481.4

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WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPS001	369.9	369.9	369.9	369.9	369.9	369.9	369.9	369.9	369.9
LPS003	600.3	363.9	0	243.7	1565.3	2624.5	1942.7	242	1892.5
LPS004	522.3	254	0	74.6	907	2638.8	1933.6	274.9	4209.2
LPS006	444.6	161.2	0	174.6	793.6	2651.4	1991.5	206.5	598.8
LPS007	528.9	136.3	0	244.9	1623.3	1202.1	2044.7	245.1	213.9
LPS008	534.5	215	0	281	1231.2	783.4	1760.3	178.5	832.4
LPS010	469	183.6	1.3	240.1	947.7	591.6	2208.3	161.2	482.6
LPS011	468.7	93.3	0	142.3	1544	1021.5	2334	254.6	1223.7
LPS012	511	278	17.7	197.2	2129.6	68.9	1362.7	478.9	960.4
LPS013	478.2	407.1	192.1	235.6	2470.6	9	1163.9	885.7	1109.4
LPS014	579.7	369.1	0	272.7	2799.6	1525.7	2222.4	606.9	2638.6
LPS015	419.7	254	0	2380.7	7188.1	4998.4	16519.6	5245.1	15550.4
LPS019	1068.4	279.6	0	396.2	3848.5	3074	3866.9	959.1	3664.7
LPS020	314.2	109.1	0	102.7	2036	234.4	1504.2	319.6	1053.2
LPS023	364.9	104.2	0	100.7	1151.8	0	1253	175.5	570.5
LPS024	804.7	213.8	0	346.3	3248.5	2523	2722.6	915	1987.4
LPS025	1374.7	407.8	0	857.1	4731.2	2584.2	4119	1138.4	2458.4
LPS026	337.6	86.1	0	100.2	1242	0	1052.9	242.9	988.9
LPS027	440.5	182.5	0	118.5	1318	691.2	1274.1	226.1	385
LPS028	369.5	166.2	0	168.7	2587.7	2597.8	4035.5	565.9	1883.1
LPS029	323.4	141.9	0	165.3	2524.3	2147.2	3031.3	567	2263.9
LPS030	362.3	226.5	0	169.6	1528.2	422.9	1236.7	239.2	1049.1
LPS031	591	536.7	4.9	383.6	1768.3	850.4	1013.3	399.8	781.4
LPS032	443.9	327.3	0	328.1	3200.9	1880.1	1832.8	265.6	1391.6
LPS036	1093	781.8	24.5	680.8	3911.3	3750.9	3746.7	661.8	3856.4
LPS037	501.6	180.4	0	200.9	2664	2369.8	1960.5	339.9	2892.9
LPS038	1180.1	471	155.9	1679.7	4392.3	2103.5	3019.9	800.3	2819
LPS040	398.8	108.6	0	103.9	1030.7	195.9	1566.1	144.4	682.1
LPS041	384	153.6	0	149.7	989.2	1257.5	2235.4	143.3	1228.4
LPS042	1381.9	951.7	44.9	716.1	3682.1	2755.7	4011.7	508.5	2963.4
LPS043	1211.6	704.8	74	613.6	3494.4	2435.3	3362.1	391.4	1544.7
LPS044	361.3	100.2	0	142.1	2244.4	3031.8	2653.5	393.4	1620.1
LPS045	285.7	75.2	0	64.4	856.5	223.5	1616.1	216.8	609.7
LPS046	325.8	217.2	0	70.2	1758.6	0	1280.9	284.9	1115.5
LPS047	2041.3	1347.8	768.4	1080.5	4169.9	3927.9	4263.5	1831.6	4804.9
LPS050	3226.4	3356.4	6064.5	3347.5	9841.4	3046	5362.2	2924.8	5821.2
LPS051	377.1	96.4	0	156.8	2452.6	2286.5	3035	396	2238.1
LPS052	330.1	80.1	0	162.6	2418.1	0	2097	352.5	1677.3
LPS053	402.6	160.1	0	146.3	2249.5	56.9	1986.1	464.3	1349.6
LPS054	497.4	147.5	0	184	2188.4	379.1	1976.1	308.6	1558.9
LPS055	1168.2	645.7	0	354.9	3901.1	1476.5	2607.5	774.8	3026.1
LPS056	1549.5	1243.3	37.9	752.6	4770.9	3403.7	4086.8	1204.2	4958.4
LPS057	387.5	154.3	0	262.7	2612.2	502.6	2317.5	365.1	1418.8
LPS058	671.2	198.9	0	434.8	4189.9	2258.6	3366.3	586.3	2190.5
LPS059	726.2	207.5	0	304.6	2974.8	2054.3	2712.8	395.1	1331.6
LPS060	534.2	215.8	0	221.7	2896.9	718.3	2693.3	477	2474.9
LPS061	530.8	369.4	0	204.3	1801.1	1286.4	1533.6	298.7	1327.2
LPS062	407.4	305.2	0	226.4	1509	0	1413.1	212.5	954.6
LPS063	619.4	280.8	0	282	3987.4	1805	2589.9	642.1	1650.4
LPS064	3689.2	4982.4	10201	3080.3	8359.8	3622.3	8304.6	2997	13781.1

LAW OFFICES
FINNEGAN, HENDERSON,
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& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPS065	466.4	189.7	117.3	817.1	4336.3	2332.6	4393.4	1092	3866.8
LPS066	269.5	104.6	0	131.4	1006.2	76.7	1834.6	185.9	668.5
LPS067	426.4	179.7	49.3	341.3	4153	4077.7	5101.3	1195.9	3894.1
LPS069	367.8	136.7	0	128	1456.6	0	2685.6	308.7	1234.3
LPS070	438.5	137.3	0.4	111.6	1932.5	25	3005.3	210.4	721.5
LPS071	283.9	83.2	8.5	109.2	1831.5	0	3634.2	302.8	708.3
LPS072	301	147.2	5.7	132.9	1600.8	592.3	3051.5	331.5	1173.5
LPS073	692.1	485	251.5	497.9	4205.3	2827.4	3777.9	740.1	3882
LPS074	36280.3	66359.2	63362.2	44047.1	47176.9	20938.9	64534.5	33666.4	78457.8
LPS075	3204.8	1250.6	650.9	1033.7	4976.3	4377.1	4632.6	1617.1	5570.9
LPS076	434.7	127.9	0	204.7	1731.3	419.1	2737.8	298.8	2175.1
LPS077	416.6	107.6	0	327.2	3360.7	1950.5	4020.1	609.1	3713.9
LPS078	5164.5	1194.3	906.3	6556.7	20779.8	7364.3	28847	8680	22339.1
LPS079	1317	501.9	304.2	893.4	5047.6	3196.6	4887.5	1058.8	4992.1
LPS080	27721.4	56038.2	70896.6	26826.4	43426.4	20557.3	47819.2	16935.5	68145.5
LPS081	36397.3	66337.3	48195.9	41685.3	46187.5	20628	66138.1	31620	78253.7
LPS083	844.6	534.2	123.6	305.3	3724.2	1699.7	2524.6	583.8	3266.4
LPS084	665	249.4	0	334.5	2570.6	1491.7	2893.2	342.8	2061.7
LPS086	456.6	155.8	0	165.1	1962.7	754.5	1931	130.2	2176.5
LPS087	967.5	450.7	17.2	633	4238	3720.3	5373.9	1754.7	19094.1
LPS088	468.4	276.1	0	151.1	1109.4	0	1779.7	302.8	2497.2
LPS089	329.2	316.9	0	133.6	988.7	0	1619.6	320.7	1616.9
LPS090	478.9	272.3	0	218	4486.4	2182.3	2923.1	584.6	2640.7
LPS091	385.7	177.9	0	290.7	2923.3	2008.6	2453.2	441.5	2246.6
LPS092	396.3	164	0	345.2	2249.1	1219.1	2906.7	413.9	1589.3
LPS093	308.3	164.5	24	98.7	262.3	427.8	2140	175.4	661.4
LPS094	331.6	179	54.2	146.4	773.3	948.2	1729.1	116	1030.7
LPS095	363.7	157.7	46.3	142.5	967.7	341.4	2639.7	199.3	1055.4
LPS096	266.9	90.6	0	59.3	676.5	0	2616.2	136.5	215.6
LPZ001	270.9	49.7	21.1	121.2	1958.2	496.8	4495.7	325.6	557.7
LPZ002	491.7	231.8	157.9	345.8	1929.4	1183.4	3243.9	305.5	932.6
LPZ003	632.6	407.2	342.3	343.5	2630.6	2108.3	3212.8	423	4663
LPZ004	2034.4	2260.7	1487.4	1442.5	5730.7	2135.4	5424.1	1804.4	5786.1
LPZ005	6301.3	4683.6	2801	10127.5	31972.9	7747.5	51335.5	17767	52067.8
LPZ006	471.7	131.2	0	179.4	1964.1	1552.2	2977.9	333.5	2954.9
LPZ007	584.6	383.7	69.3	294.3	1424.1	531	2664.9	265	3021.7
LPZ008	325.4	87.5	14.4	176.8	1966.6	1588.5	2420.1	199.5	3481.2
LPZ009	451.3	281.6	143.4	362.3	3149.2	4280.4	3006.5	357.5	4395.9
LPZ010	1324.5	1442.8	621.8	931.8	4310.4	3238.7	3926.9	617.4	4912.5
LPZ011	1740.9	2073.5	1436.2	1075.8	4631.4	5232.7	4563.3	1080.6	5456.6
LPZ012	424.4	217.8	50.1	271.8	2286.7	713.5	1791.4	390.6	3209.9
LPZ013	395.4	123.8	33.1	181.1	3456.8	2121	2898.4	428.9	2673.3
LPZ015	490.7	210.7	60.8	130.8	2889.2	330.5	2123.4	230.2	2680.6
LPZ016	2411.9	710.9	346.5	1201.2	6897.9	4057.6	13340.1	3246.1	16664.2
LPZ017	635	257.4	36.2	247.2	2797.3	1219.1	3508	558.7	3953.8
LPZ018	1405.4	474.9	214.9	3188.7	8143.7	4992.8	12908.9	4208.2	14318.9
LPZ019	3487	975.9	698.4	8916.5	23680.5	15131	31656.3	14191	45343.3
LPZ020	251.9	195.6	0	40.9	1448.5	860.4	1113	305.5	971.2
LPZ022	250.1	112.4	0	133	2085.9	1282.5	2538.5	532	613.2
LPZ023	355.5	122.6	22.9	47.8	224	879.4	1419.1	132.3	605.4

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FINNEGAN, HENDERSON,
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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPZ024	366.5	108.9	45.7	94.8	225.3	723.1	1276.8	81	319.5
LPZ025	705.4	278.6	202.1	716.7	5145.5	4563.4	7215.5	1581.9	4195.8
LPZ026	268	100.6	9	92.1	1164.5	750.4	3973.6	275.5	642.3
LPZ028	386	174.2	96.8	374.9	4188.4	2733.8	7024.6	1186.8	2375.6
LPZ029	221.9	86.8	0	47.8	225.3	264.4	2172	162.4	957
LPZ030	319	166	67.6	146.9	801.6	1385.4	2283.4	145.8	1189.4
LPZ031	2010.6	881.7	538.1	754.3	4625.8	3395	4051.7	1327.9	5202.1
LPZ032	36097.5	35972.1	13659.1	19975.4	45544.5	20035.8	63759.8	31117.4	78268
LPZ033	1813.8	433.6	243.7	1171	7402.4	2278.7	10670.5	2204	5643.8
LPZ034	332.6	97	34.6	181	1097.2	0	2704.1	262.6	3481.4
LPZ035	248	60	0	71.4	1188.8	0	1332.5	153.6	3028.4
LPZ037	375.8	133.8	0	114.6	3024.3	909.1	2350.6	248.2	3546.8
LPZ038	577.7	237	44.3	370.7	4484.6	3572.5	4266	907.9	4571.4
LPZ039	965.6	406.7	361.2	537.9	4020	2304.1	4269.9	816	3717.5
LPZ040	399.9	127.4	0	88.3	1200.5	365	2123.2	244.3	1955.4
LPZ041	318.4	105.1	0	136.6	856.3	716.6	1528.5	245.6	1538.5
LPZ042	289.3	77.6	0.9	189.5	441.5	365.4	1007.7	239.2	1212
LPZ043	417.3	166.7	57.4	158.2	1197.2	1617.9	793.5	569.1	2018.7
LPZ045	754.8	310.3	152	691.5	4810.4	3305.3	4043.7	1476.3	3925.7
LPZ047	270.5	155.4	53.1	39.1	2165.6	579.6	980.9	361.7	1036.3
LPZ049	809.6	381.9	0	461.4	4406.4	2277.4	4764.6	2257.8	5528
LPZ051	333.1	121.5	0	56.6	1597.8	1677.8	891	270.7	1134.6
LPZ053	271	119.7	0	16	1662.4	2447.8	1202.4	201.1	827.1
LPZ054	345.4	131	61.7	79	1181.1	2238.5	1426.5	156.5	627.5
LPZ055	291	78.1	102.9	63.5	551.3	2343.8	1433.5	193.6	814.2
LPZ056	364.6	167.9	83.6	130.3	1816.9	2580.4	2589.4	343	1579.8
LPZ057	250	76	0	11.9	426	457.6	2589.6	113.4	709.8
LPZ058	231.1	40.8	6.2	44.4	454.7	163.4	3403.4	208.5	1300.4
LPZ059	239.2	78.6	0	15.7	189.7	267	3272.7	141	1439.2
LPZ060	235.1	26.7	29.4	35.6	524.8	1238.2	2231.2	182.5	1908.8
LPZ061	402.1	268.4	141.6	254.6	1694.1	3088	2343.5	557.3	4157.7
LPZ062	727.7	146.8	0	203.3	2873.3	2418.9	3109.6	926.6	5812
LPZ063	316.7	108.2	25	190	1837.3	1025.1	2727.2	421.8	4195.9
LPZ065	512.5	59.9	94.9	583.5	5694.4	3741.6	5366	1221.6	3911
LPZ066	622.2	66.8	23.8	405.6	6932.1	3089.5	4804.9	642.2	4079.9
LPZ067	883.7	218.7	0	358.7	4518.2	2342.9	5200.8	1318.4	5539.6
LPZ069	335.6	100.2	0	46.8	0	0.7	1736.5	255.4	2910.4
LPZ070	422.6	143.3	49.6	168.8	1231.5	1170.6	2432.2	262.7	2122.5
LPZ071	356	71.9	0	299.7	2303.6	1909.8	2575.9	447	2827.6
LPZ072	206.5	32.6	0	71.7	0	0	1362	189.6	907
LPZ073	374.2	129.6	32.1	125.8	307.4	691.8	1617.6	282.4	1306.9
LPZ074	434.7	86.5	0	76.6	1671.1	0	1112.5	232.7	663.5
LPZ075	298.5	173.5	0	53.5	4083.2	0	1143.9	113.7	335.1
LPZ076	209.9	83.1	7.2	7.4	2185.9	0	490.5	226.6	362.9
LPZ077	813.4	558.3	0	339.1	3733.4	4279.8	1115.9	671.7	4136.8
LPZ078	532	349.8	0	265.8	4460.1	3290.7	2776.8	686.3	3283.3
LPZ079	347.8	183.6	11.6	53.3	2115.4	1191.7	1451.2	160.5	1233.2
LPZ080	948.1	264.9	178	455.1	4633.9	2869.1	4230.5	1378.5	5566.5
LPZ081	313.7	96.1	100.2	59.7	1161.6	1470.2	1119.7	98.5	710.9
LPZ082	260.9	120.3	18.4	68.3	1734.5	1430.6	1581.6	160.1	379.4

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& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPZ083	284.9	134.6	12.6	7.8	1067	906.1	1482.7	107.2	790.5
LPZ084	1493.3	437.1	0	788	4497.3	4608.3	5078.9	2267.8	5087.7
LPZ085	468.1	139.4	0	62.1	1618.8	1355.9	4314.9	340.5	2421.5
LPZ086	601.3	91.6	11.9	332.9	3540.3	3354.6	6675.2	781.2	5545
LPZ089	457.1	124.1	26.2	267.7	2378.1	3364.6	3390.2	448.7	2930.7
LPZ090	436.6	50.7	0	149.1	3135.3	2087.8	3090.4	483.8	3408.1
LPZ091	350.2	91	96.2	99.2	1524.3	1976.3	3215	315.9	4532.8
LPZ092	387.6	33.6	0	114.4	2386.7	2600.9	2845.7	274.6	2036.7
LPZ093	195.6	25.8	0	27.1	2343.1	321.7	2875.2	252.7	1428.2
LPZ094	274.8	42.8	0	35.2	886.9	0	2502	152.6	1571
LPZ095	288.6	91.5	0	14.1	3.5	0	2317.2	144.4	1427.4
LPZ096	475.4	138.7	13.1	199.2	1690.8	1415.2	3939.2	207.2	1889.7
LPZ099	428.1	73.8	0	185	2531.8	2596.6	3925.9	399.8	1967.5
LPZ100	474.3	131.1	24.6	266.6	2710.6	2276.7	3358.6	503.5	2245.1
LPZ101	492.1	101	81.9	233	2341.4	2076.1	2199.9	423.1	2022.4
LPZ102	477.3	133.2	0	167	3722.9	1604.4	2432.1	386.5	1199.8
LPZ103	353.5	90.7	0	108.9	4756.8	214.4	1447.5	203.9	760.7
LPZ106	534	199.4	58.6	117.6	3052.4	1259.2	1610	277.6	1224.3
LPZ107	29718.3	56194.4	31132.5	35651.5	44972.5	20589.6	38396.3	32828.7	75965.1
LPZ108	852.4	433.1	161.4	417.4	4354.8	2259.1	3536.9	1168.5	3161.8
LPZ109	554.2	248.6	83.8	254.6	3303.4	2521.1	1972.8	608.5	2858.5
LPZ110	614	203.3	166.1	182.1	3236.7	2792.6	2764.1	455.5	3139.2
LPZ111	349.5	167.7	77.4	82.9	1407	1386.1	1469	200.9	1397.5
LPZ112	497.3	279.2	65.3	242.6	3553.5	2504.1	2454.6	328.3	2182.2
LPZ114	890.2	346.7	0	399.3	4520	3367.9	2902.7	1229.6	3474.1
LPZ115	24782.8	12016.1	1401.9	12188	32718.2	17087	38203.9	17191.1	25318.5
LPZ116	1388.1	392.7	0	884.6	8895.4	3131.2	15554.1	2195.7	5401.6
LPZ117	6228.4	4810.2	389.7	1298.8	4199	2671	5473.5	1488.2	3911
LPZ118	424.5	267.3	39.9	196.2	2507.4	2210.1	2856.3	370.3	2640.4
LPZ119	295.1	183.4	0	59.8	2443.3	1153.2	2040	158.7	1132.1
LPZ120	213.5	88.4	49.2	185.9	1336.6	1390.4	1604.5	186.7	1360.8
LPZ122	317.6	120.3	0	92.1	1390.2	2045.1	1701.2	112.5	1307.5
LPZ124	346.6	173.2	38.9	119.4	2097.9	543.9	2679.2	221	1941.7
LPZ126	436.1	185.4	0	142	1762.2	0	2164	283.2	2343.6
LPZ127	455.7	208.6	0.1	109.8	1091.7	1925.5	3143.4	345.4	2565.8
LPZ128	421	602.3	25.1	651.1	4496.3	2712.3	5456.8	1177.7	3875.7
LPZ131	287.1	401.2	0	58	1931.2	422.4	3510.2	232.2	1275.8
LPZ133	377.8	399.9	141.9	139.5	2396.5	1989.9	4287.5	388.9	1119.6
LPZ136	455.2	191.7	103.3	239.9	2289.7	1775	2586.1	322.4	1429.8
LPZ137	398.1	123.1	0	214.7	2480.2	1118.7	2138.5	411.3	1935.9
LPZ138	1987.8	1102.2	11.9	1112.7	4785.6	4242.8	3044.7	1298.3	2786.7
LPZ140	401.4	205.9	115	316.7	2737.2	1950.6	1491.6	414.2	2031.4
LPZ141	917	621.2	0	726	4938.4	3889.9	3237.4	1109	4165.8
LPZ143	4702.9	1483.9	774.8	6791.2	20187.4	6913.4	23175.5	10795.1	26322.7
LPZ144	529.7	392.6	25.7	303.5	2644.9	1902.4	2380.9	486	2422.7
LPZ145	410.2	206.5	25.4	152.3	1618	2219.1	2012.8	357.8	2494.3
LPZ146	294.2	152.3	0	125.3	1063.5	1142.1	1129	215.1	1927.1
LPZ147	366.5	238	0	246.5	2120.4	956.1	1343.4	260.2	1539.3
LPZ148	390.6	212.9	0	170	2107.1	2195.4	1832.6	1240.9	3839.8
LPZ149	1872.8	1139.7	218.5	1748	6204.2	1641.3	5144.7	3526.5	5193.6

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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPZ150	1958.1	1284.1	645.6	10615.2	29419.9	2976.7	52052.2	21478.7	41125.9
LPZ151	3477.3	1936.4	155.4	1423.9	5253.1	1925.1	5434.9	2248.3	5180.5
LPZ152	963.2	481.9	42.2	658.9	4770.8	3607.7	4661.8	1003	4661.9
LPZ153	13685.9	27883.7	11205.9	13827.1	24872.9	15412	26204.7	12163.3	41713.9
LPZ154	621.9	470.5	45.6	381.1	2965	2584.3	2802.2	416.8	2738.4
LPZ155	2004.5	1513.1	388.4	1358.9	4265.3	4159.3	4386.4	1022.6	4543.9
LPZ157	2978.4	1332.8	407.8	1400.6	4650.6	3692.3	4760.8	1195.9	5002.5
LPZ158	12352.4	18933.2	12155.7	9376.4	23120	15280.6	18384	10293.8	50995.4
LPZ162	3778.2	4069.3	426.4	2285.5	6458.4	3004.6	5794.3	4161.4	13171.9
LPZ165	1181	805.1	0	756.4	4641.9	2702.4	5464.6	1470	4822.6
LPZ166	4624.9	5016.4	0	2508.8	9907.8	1939.3	5655.3	2999.9	5667.6
LPZ167	3339	1655.9	319.8	1101.8	4807	4980	4678.8	1968.2	4248.1
LPZ169	787.5	556.1	226.4	461.9	2830.2	2225.4	3549.7	684.4	3249
LPZ170	851.1	501.5	0	589.6	4405.2	4440.6	4652.4	1622.7	4556.9
LPZ171	1325.6	612.2	0	697.6	3647.5	3148.7	3446.8	1053.8	4043.4
LPZ172	748.6	490.4	0	802.4	3953.2	2939.1	3550.9	848.3	3809.5
LPZ173	4460.6	3415.7	1050.1	5769.8	16078.4	6658.8	16861.6	8623.4	21007.1
LPZ174	501.9	308.6	36.2	358.6	3054.1	1731.2	1954.9	862.9	2773.9
LPZ175	1476.5	1057.1	181.6	836.9	3731.4	3120.9	3879.4	755.9	3687.2
LPZ177	302.3	228.3	18.6	107.1	753.6	1430.4	941	165.4	1411.2
LPZ179	616.8	314.9	8	379.4	4544.7	2954.4	3425.3	1361.5	5310.3
LPZ181	1103	430.7	0	671.3	4917.1	3821.3	4976.3	2646.1	5785.8
LPZ182	992.8	435.1	0	468.1	3930.1	4177.6	3287.5	909.9	4820.2
LPZ186	2455.7	1428.7	760	2414.4	9679	4431.1	5537.9	3859.3	5921.7
LPZ189	40770.3	68311.4	75133.7	45673	47303.1	21072.6	66542.7	34849.1	78485.4
LPZ194	612.8	572.1	155.6	376.3	3673.5	2240.2	3365.2	469.5	3608.6
LPZ195	676.9	346.6	32.5	459.9	4278.1	4622.4	4442	1006.8	4754.3
LPZ196	2923.1	1787.1	448.6	1537.1	4490.3	3684	4875.6	1426.9	4447.8
LPZ197	592.3	177.5	343.1	629.4	5825.4	3639.7	4308.7	649.9	2838.2
LPZ198	801.7	295	8.2	511.1	4384	3156.4	4823.8	1125.6	3947.2
LPZ199	402.5	165.1	62.7	265.9	2158.3	2363.7	3531.7	423	2360.1
LPZ201	1338.5	361.2	209.6	1053.7	4997.8	4565.6	5107.6	2350.9	5882.2
LPZ202	8178.9	2795.3	2359.9	12950.9	39890.9	20247.9	62085.4	31826.4	78541.6
LPZ203	1983.5	1083.8	1146.8	2044.1	9173.9	2174.8	11135.5	4073.8	19571.3
LPZ204	38154.8	66241.1	88440.7	45372.1	47166	21054.3	65826.6	33875.6	78581.7
LPZ205	1079.5	521.7	589.1	758.4	4742.5	3837.7	5220.2	1453.2	4888.6
LPZ206	947.6	700.1	505.1	697.8	4089.6	2774.1	5242.9	1190.3	4578.7
LPZ207	39899.6	60813.3	95637.5	45997	47123.6	21073.2	63996.4	35149.4	73080.5
LPZ208	27268.6	27230.4	39428.3	29579	40216.5	20480.2	42465.8	26526.9	76872.4
LPZ210	683.8	538	429.6	439.8	2402.5	3285.4	2419.1	636	3965.6
LPZ211	603.1	530.3	87.2	434.6	3653.3	2234.5	1744.1	359.8	1644.7
LPZ212	1018.4	580.7	155.2	1734.1	9212.3	2338.9	5061.9	2257.3	4303.3
LPZ213	465.6	327.1	33.1	296.6	3012.3	2419.4	2198.4	570.9	2013.9
LPZ214	245.6	267.4	0	160.5	912.5	756.5	880.7	133.9	936.8
LPZ215	981.1	492.8	52.3	828.3	5390.6	4771.4	4868.1	2893.1	15622.6
LPZ216	9410.5	3834.8	1843.2	14492.9	43137.1	21097.9	63778.6	34830.7	78538.8
LPZ217	31119.9	47126.3	30689.1	28515.4	38695.3	19884.5	37913.9	21282.9	69590.2
LPZ219	1300.2	886.5	475.3	946.3	4898.3	4361.6	3705.4	1784.6	5810
LPZ220	5695.5	7233.6	9375	4579.9	6540.8	4340.1	5612.6	2993.6	5852.3
LPZ221	242.6	209.5	0	186.3	2553.4	2132.5	1632.9	258.2	3202.9

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FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPZ222	186.9	130.5	0	163.4	2138.4	1386.3	1855.4	223.3	2407.6
LPZ223	289.9	168.4	0	164	2019	1582.7	2374.4	250.3	2309.2
LPZ224	308.3	114.3	20.5	333.9	2467.7	2535.2	2722.9	518.9	3054.9
LPZ225	5540.8	1287.2	919.3	7087.6	18926.6	9277.7	20292.9	8705.5	19974.7
LPZ226	179.1	111	9	136.8	1049.8	2071.1	3332.8	463.4	2517.8
LPZ227	243.5	136.2	0	341.4	2502.5	2597.6	4869.5	3226.2	16356.7
LPZ228	470	249.6	0	349.2	4062.6	3388.6	5688.3	2586.2	15112.1
LPZ231	480.4	296.3	87.4	326.6	3832.4	2343.1	5557.3	1542.5	5679.2
LPZ233	468.6	332.9	161.7	350.3	2519.3	1967.1	5201.8	996.1	4833.8
LPZ234	525.8	368.6	287.8	380.3	1626.6	1285.8	4231.8	1235	5329.5
LPZ235	310.7	233.3	0	370.2	1746.3	1474.1	4135.8	541.1	3382.9
LPZ237	683.5	468.8	487.2	506.9	3683.2	2108.7	3966.8	1369	5254.5
LPZ239	546	192.6	339.2	331.5	2584.8	2384.8	3215.7	754.4	4041.1
LPZ240	353.7	280.8	163.9	274.8	2281.8	1696.4	2345.8	319.2	2180.8
LPZ241	283.3	260.2	0	206.4	2481.1	1787.8	775.1	426	1729.3
LPZ242	7478.4	2664.4	1039.1	7024.1	22393.3	11120.5	20928.9	8581.6	22951.9
LPZ243	242.4	167.1	0	157.2	2175.8	182.4	806.9	237.7	977.2
LPZ244	350.3	206.1	0	409.4	4522.7	3997.1	4486.3	1022.8	3387.1
LPZ246	260.9	200.9	0	251.8	1930.9	1335.1	995.1	1033.7	4712.9
LPZ247	438.3	274.4	0	341.4	2994	2325.3	2926.7	1508.7	5494.3
LPZ248	748.4	714.1	291.3	878.4	3814.2	2737.7	3489	1155.1	4689.5
LPZ249	373.3	375.6	0	613.1	4798.1	2088	3560.8	433.5	2486.3
LPZ250	159.5	201.7	0	317.6	2037.8	2085.9	1721.8	220.5	2051.7
LPZ251	141.7	157.9	0	178.9	1377.4	1723.8	1136.8	91	1271.1
LPZ255	220.8	176.1	0	646.5	4160.8	2725.5	5110.3	1217.2	5217.7
LPZ256	94.6	101.7	0	149.5	821	812.6	1989.5	65.4	432.2
LPZ257	147.9	118.4	0	135.1	1206.9	1208.1	2197.2	207.9	745.8
LPZ258	168.3	124	0	174.7	2264	2172.4	2672.8	532.8	2245.2
LPZ260	213.5	172.9	0	141.3	1172	2974.6	4118.3	232.4	1057.4
LPZ261	147.2	78.5	0	126.6	1212.5	2349.9	4604.9	139.4	741.6
LPZ264	318.3	174.1	0	201.7	3104.4	2387.6	5505.8	582.7	3775.1
LPZ265	1566.8	449.9	129.7	646	4992.3	3477.7	5635.5	988.7	4307.2
LPZ266	92.8	287.2	0	132.5	931.4	0	4689	190	726.3
LPZ268	171.3	217.2	0	206.8	2142	2135.8	5156.3	296.8	1912
LPZ269	1530.1	571.5	419.3	2333.1	11130.7	4947.4	13881.5	5155.2	5755.6
LPZ270	162.3	291.4	0	450.4	3822	3736.4	4342.8	978.4	2987
LPZ271	454.6	266.6	45.9	381.8	3194.7	2859.7	3598.7	1277.5	4054
LPZ272	2943.2	763.9	613.2	1451.3	7894.9	2900.8	5222.6	3222.4	16317.5
LPZ273	215.5	178.7	0	112.2	1288.3	908.3	145.5	182.5	544.8
LPZ274	271.5	189.3	0	322.8	3311.7	1141.5	1301.4	620.8	3182.2
LPZ275	174.5	152.8	0	99.6	1052.3	0	0	109.3	887.1
LPZ276	146.8	139	0	129.4	1165.3	123.5	505.4	82.6	461.9
LPZ277	201.8	137.5	1.8	57.1	761.5	931.9	497.5	106.1	1427.3
LPZ278	177.9	152	0	76.6	588.2	1424	311.2	107.3	1178.8
LPZ279	183.3	179.3	0	304.9	2458	1032	524.7	276	1530.9
LPZ280	142.1	125.5	0	125.6	1116.5	623.5	1147.9	125.4	770.5
LPZ281	18	109.8	0	58.9	563.4	850.5	564.6	11.5	317.8
LPZ282	54.3	164.1	48	95.5	1493.6	1874.9	1033.3	54.7	844
LPZ283	1607.8	392.6	48.4	1220	6358.1	2922.6	5552.8	1970.3	5032.3
LPZ284	42.5	119.4	0.3	48	804	748.4	1365.8	66.6	0

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FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPZ286	34.3	164.5	0	74.8	973.6	1463.4	1205.7	81.2	329.3
LPZ287	118.8	186.4	0	116.4	1573.7	1568.6	2124	252.9	884.4
LPZ288	103.4	162.8	0	78.3	1328.1	2890.4	4192.3	196.9	598.1
LPZ289	137.1	87	0	113.6	2096	2101	5147.9	332.3	913.7
LPZ290	1598	425.5	186	1782.8	10543.9	4598.5	16706.4	3923.8	5648.6
LPZ293	155.8	225.7	0	129.9	3228.2	2291.5	4891.2	316.9	2001
LPZ294	65.5	180.6	0	66.6	2237.5	527.7	4397.4	127.5	688.2
LPZ295	119.9	258.8	0	149.7	1964.6	560.6	5062.1	141.5	897.3
LPZ297	333.9	277.6	59.4	830	5667.2	3950.7	5680.5	1452.6	3614
LPZ299	102.6	225	12.2	268.1	734.7	898.2	4025.5	371.2	913
LPZ300	231	271.7	97.1	42.6	113.2	1713.7	3264.5	4295.2	631.1
LPZ301	272.7	378.2	155.6	97.2	77.2	2110.4	1733.8	485.6	1392.8
LPZ303	145.6	184.3	641.8	52.8	1562.5	1072.8	365	55.5	358.3
LPZ304	422.5	346.5	108.2	350.8	3262.7	2215	1102.8	264.1	1534.7
LPZ306	2207.6	484.7	609	3182.2	9671.4	3639.8	17157.3	3556.4	15015.7
LPZ307	1761.1	1119.4	454.7	846.1	4114.9	2673.3	4082.5	554.8	2983.5
LPZ308	153.5	213.5	85.5	113.3	1369.9	1433.3	133.8	123.2	1146
LPZ309	132	192	14.3	49.2	1137.6	1626.7	126.9	85.1	805.1
LPZ310	325.9	353.6	311.3	253.1	4210.4	2703.3	1846.5	513.3	3102.9
LPZ311	176.9	217.7	72.3	245	3652.2	4352.6	4175.7	734.7	4625.7
LPZ312	70.4	177.2	139.4	53.2	2094.2	1461.1	945.5	57	274
LPZ314	247.5	221.2	217.2	66.9	1767	753.8	872.4	93.1	751.2
LPZ315	167.6	220.4	322.5	172.9	3442.4	1985.7	2505.1	698.5	3667.7
LPZ318	912.5	297.8	441.9	957.6	7473.1	2682.6	6826.4	2471.8	5148.9
LPZ320	7.3	212.8	154.8	55.8	1682.1	1548.5	1038.5	111.1	822.5
LPZ321	199	259.6	157.2	96.8	2588.8	2465.4	3436.8	409.2	3989

LAW OFFICES
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202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPS001	369.9	656.8	1322	4095.5	4733.4	7892.2	3248.2	5064.2	6260.9
LPS003	442.5	392.9	262.1	648.7	2035.7	570.6	4524.4	1332.8	543.9
LPS004	811.4	552.2	515.2	1694.9	2438.2	425.1	1218.8	714.3	86.8
LPS006	271	141.2	200.2	0	662.1	1245.1	261.5	1282.6	405.7
LPS007	212.1	91.8	139	47.7	243.4	0	929.2	568	267.1
LPS008	197.6	196.8	224.7	0	235.1	2144.5	1034.5	985.2	307.3
LPS010	152.7	133.4	253.8	241	299.5	1667.7	242.1	1218.8	1170
LPS011	186	136.1	257.9	816.5	257.4	2372.2	77.7	1377.7	1346.8
LPS012	317.2	238.4	236.4	817.5	1316.7	1626.1	0	1324.1	564.7
LPS013	349.5	403.6	412.9	1840	1582.6	2769.8	215.4	1196	1328.8
LPS014	511.4	1574.1	257.3	4169.4	5035.7	4543.5	1016.4	3744.8	3779.2
LPS015	2495.9	3076.7	1720.8	7899.3	3640.5	7103	1228.1	5376.7	11989
LPS019	1028.2	604.5	239.7	3074	2189.3	2161.1	1239.9	2955	2426.7
LPS020	324.1	222.9	120.5	1214.3	1056.8	676.2	872.7	916.8	1058.1
LPS023	160.9	116.3	50.3	623.9	1984.1	0	640.7	349.7	694.3
LPS024	359.3	324.3	198.9	1596	2789.8	1253.1	1212.2	2644.1	3158.3
LPS025	614.7	616.8	493.6	3452.4	3736.3	3726.5	1796.1	4133.4	5569.5
LPS026	153.7	494.7	0	3053.4	3077.5	2157.2	806.2	3886.5	2133.1
LPS027	132.2	267.1	0	1309.2	2323.4	1330.2	1501.6	1931.3	1355.1
LPS028	214.3	446.5	155.7	2472.5	3336.1	2467.9	2987.9	4507.5	3530.8
LPS029	202.7	384.3	223	2040.4	2060.5	2600.8	7214.8	4150	3867.7
LPS030	113.5	132.5	0	515.6	2793.9	110	2158.7	2684.7	1237
LPS031	168.7	123.5	11	557.6	3086	812.5	6212.6	2534.1	3290.9
LPS032	145.2	160.9	1.7	650.5	2144.2	1070.8	1474.2	2819	3561.4
LPS036	582.6	616.4	200.9	2224.2	2656.4	1723.6	3073.1	1866.1	2955.4
LPS037	502.6	620.4	219	1626.6	3359.2	2705.7	2125.3	2456.9	2004.1
LPS038	962.6	216.5	375.7	0	1256.5	930.9	1492.9	1578.3	1406.9
LPS040	228.9	86.1	158.6	0	256.8	0	245.1	758.3	1.7
LPS041	222.7	149.2	123.3	0	252.4	0	965.1	1065.9	553.4
LPS042	447	661.1	489.9	1672.8	2520.7	492	1046.8	2834.7	1940
LPS043	333.7	264.6	407.3	656.8	1046.4	546.5	1412.3	1097.9	948.4
LPS044	249.8	277.8	652	1327.3	907.5	1110.5	1892.3	1353.4	1674.8
LPS045	250.7	107.2	177.9	302.6	231.9	944.7	1881.7	0	485.4
LPS046	232.4	285.6	224.5	1302.1	1872.6	1104.6	2610.7	1128	1744.2
LPS047	2649.2	6969.7	2792.6	14436.1	10141	5428.8	4057.3	2999.2	13647.7
LPS050	2428	7502	3442.1	12204.8	7385.4	9850.6	3395	8052.4	14726
LPS051	478.2	219.7	175.1	1861	2222.1	1876.9	1922.5	800.9	2052.9
LPS052	328.2	196.2	138.3	984.6	1458.3	1324.4	1585	1112.9	1726
LPS053	264.2	111	0	1370.2	1524.9	1548	2692.1	2941.5	3096.1
LPS054	285.4	231.1	8.5	1370.4	2138	1273.8	2930.8	2762.2	2604.2
LPS055	1192.2	1118.8	180.5	5840.8	4203.1	3690.8	1865.1	3205.9	4824.3
LPS056	1541.6	2959.9	1354	9519.2	8084	6331.3	1820.6	5902.8	11668.9
LPS057	214.5	406.9	0	2028.8	2744.4	756.5	2136.1	1844.8	2454.6
LPS058	277.4	244.5	70.8	1623.9	1826.1	1626.5	2708	2514.4	4077
LPS059	115.3	135.2	1.5	996.9	1194.7	1022.8	1723.1	1265.3	2390.7
LPS060	163.3	268.5	0	1866.5	1707.3	1953.7	2184.7	2422.6	2990
LPS061	222.7	255.6	53.4	1448.5	2146.6	1600.7	1956.2	2511.7	3332.5
LPS062	136	228.5	99.1	627.1	863.2	467.7	1610.3	2304.9	2842.2
LPS063	299.7	251.8	226.3	796.8	1427	1771.5	1174.1	930	1433.9
LPS064	3079.8	4014.9	3039.3	7349.2	10807.8	7372.1	10515.8	4426.8	13038.7

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FINNEGAN, HENDERSON,
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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPS065	434.1	644.6	313.7	1147	1456.3	3097.5	2632.9	3695.2	1575.1
LPS066	214.7	171.7	134.2	0	69.3	249.7	726.1	871.9	586.6
LPS067	706.6	686.2	488.8	3013.5	2498.9	4522.1	4844.3	4782.1	5775
LPS069	199.6	172.1	123.9	75.4	19.4	269	874.1	854.6	0
LPS070	143.6	186.9	117.9	289.4	685.5	222.6	528.3	582.6	322.6
LPS071	180.4	170.2	187.2	157.2	183	882.3	326.7	508.4	310.2
LPS072	235.9	170.8	169.6	449.9	290.5	777.5	456.3	283.3	479.2
LPS073	900.4	1318.7	629.3	3416.1	4420.4	3894	4010.1	3367.3	4106.8
LPS074	27858.2	33812.3	32162.2	44513.2	111430.2	87262.8	47575.8	18233.4	66903.6
LPS075	2119.6	3296.9	1347.3	9540.3	5518.1	6367.8	10437.2	4054.1	9821.4
LPS076	347.6	336.3	218.5	2343.7	2326.5	1569	2415.2	1580.7	1990.4
LPS077	568.1	612.4	550.1	2908.9	1727.9	1660.2	2164.5	1798.6	2588.1
LPS078	3174.9	3137.6	3222.6	7616.1	6945.1	9024.5	11397.6	7995.6	26362.3
LPS079	1049	1066.4	302.2	4400.8	4126.8	4404.7	8203.7	4645.6	9377
LPS080	21208.7	28180.7	9065.4	39068.1	63741.1	37523.8	35948.5	11444.8	57266.6
LPS081	27381	33419.5	10292.3	43529.2	63629.5	28119	42128.9	15984.6	62043.4
LPS083	711.4	825	64.8	3306.9	3733.1	1898.2	3688.2	3407.5	3959.9
LPS084	216.4	211.2	21	1350.5	1724.2	1394.5	1965.6	2089.4	3604.5
LPS086	185.6	214.1	0	1808.2	1476	2915.6	2342.5	932.2	3339.1
LPS087	3404.7	5840.3	4144.1	12101.2	12860.9	14601.5	24953	5018.8	19643.5
LPS088	165.2	224.6	62.5	1497.7	2813.8	1593.8	3740.9	4017.3	3934.9
LPS089	223.8	213.7	0	1318.9	1574.5	2141.4	2443.5	3799.4	4185.6
LPS090	398.7	693.2	142.2	2593.7	2695.2	3465	3755.9	3638.7	3587.8
LPS091	391.2	700.6	270.7	1469.2	2092.2	3047.2	3754.2	3524.1	3149.7
LPS092	286.1	376.1	254.9	235.2	433.1	1353.8	1747.8	2658.1	3246.6
LPS093	185.6	273.7	126.3	114.7	296.8	254.7	412.1	1076.9	483.7
LPS094	232.8	261.8	151.7	274.3	249.9	641.1	891	577	1102.1
LPS095	199.3	191.7	91.4	25.7	169.9	433.7	813.4	1394.3	807.7
LPS096	97.9	139.2	63.2	0	162.4	159.2	504.6	752.3	150.6
LPZ001	150.8	207.8	257.7	202.6	485.5	704.2	555.2	1924.3	528.5
LPZ002	154.6	167.7	323.6	937.4	717.4	755.6	1068.8	1089.8	1107.7
LPZ003	1348.1	1781.1	609.3	5019	4261.6	6148.5	5600.4	3419.6	4858.4
LPZ004	2798.4	5533.1	2921.8	10703.8	8020.5	9958.4	10424.8	4135.9	14742.8
LPZ005	8403.4	19547.7	8589.6	32699.4	31426.9	21580.2	19437.9	8059.6	14660.3
LPZ006	360.6	2106.1	1173.8	7812.9	7966	11310.2	10516.8	4661.6	4618.2
LPZ007	272.5	409.9	454.7	2038.3	1107.6	2043.7	2073.5	2249.9	2751.3
LPZ008	207.7	258.2	212	1939.1	1482.6	1926.1	2243.5	1036	3324.9
LPZ009	745.1	496.5	633.9	4276.8	7474.5	9130.4	9814	5721.3	14116.8
LPZ010	893.7	1464.1	326.6	3759.5	4034	4261	4672.2	4388.6	9625.3
LPZ011	1829.5	2488.7	350.4	5922.7	4285.4	2984.2	5579.8	4236	9972.7
LPZ012	227.8	289.9	28.6	1885.9	1660.5	843.6	1913	1434.5	2785.5
LPZ013	247.7	213.8	84	1553	2015.3	1547.3	2567.6	3196.5	4347.7
LPZ015	261.7	315.8	55.6	2254.3	2409.8	2190.1	2562.4	1291.2	3237.3
LPZ016	2750.3	2151.8	3003.8	8316.2	6689.1	9147.4	9444.8	3349.6	8167.8
LPZ017	582.2	701.3	227.4	3830.1	3650.3	3828.2	4552.3	4574.5	4476.8
LPZ018	2867.6	6184.2	2746.8	10513.4	9443.1	10880.7	12748.3	5491.2	19422
LPZ019	7551.3	15875.3	9232.8	20440.4	22870.4	31026.1	33842	12823.6	38075.4
LPZ020	293.1	896.2	143.1	1661.8	2519.9	2987.1	4132.4	4022	3145.1
LPZ022	213.3	493.5	173.5	82.5	467.8	1355.1	1041.1	1481.9	1035.5
LPZ023	191.2	616.7	118.1	78.4	184	955.2	516.3	1254.6	574.4

LAW OFFICES
FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPZ024	142.6	321.7	118	0	81.9	826.8	195.8	763.9	491.7
LPZ025	661.9	764.4	536.9	1885.6	1791.8	3200.6	3017.8	4028.4	3897.8
LPZ026	194.7	221	150.4	1102	513.6	1714.4	1291.2	1625.6	980.7
LPZ028	301.3	424.2	210.9	1467.7	1654.3	2848.4	1937.1	4092.7	3086.2
LPZ029	132	151	124.8	319.5	644.1	478.7	452.4	564.8	709.3
LPZ030	305.3	616.6	170.6	2800.7	2572	2485.4	1960.4	1425.4	2381.1
LPZ031	1945	3098.6	3636.7	12422.3	7673.2	8643.5	11552.7	4295.4	4600
LPZ032	26761.5	33518.4	33623.2	45482.1	106536.1	114284.5	46968.1	16371.6	42282.1
LPZ033	2068.3	1779.5	6651.8	7887.8	5249.8	9848.7	7632.1	4500.7	7710
LPZ034	221.4	363.3	216.3	2503	1949.2	1674	2078.9	1428.3	1774.9
LPZ035	110.7	156.8	85.2	836.6	512.1	1355.7	1217.4	294	1525.3
LPZ037	229.5	206.2	186.5	1422.1	1962.7	2742.9	3023	614.1	2895.5
LPZ038	605.7	722.8	352.5	3551.8	3072.2	3614.2	3266	2494.6	4039.7
LPZ039	366.4	964.6	177.1	3755.2	2744.9	4599.4	3589.7	2407.8	3925.2
LPZ040	185.6	278.3	100.8	2131.2	1321	1479.7	1654.6	773.7	2087
LPZ041	119.9	120.8	5	1199.8	1220.8	1090	1431.2	630	2206.1
LPZ042	61.9	121.9	2.6	731.4	1897.5	986.4	1366.1	458.4	2625
LPZ043	357.9	355.1	0	3236.5	2746.8	2960.1	3138.2	911.1	3345.6
LPZ045	738.6	1003.7	565.3	3866	3168.1	6406.2	4028.7	4526.2	4573.4
LPZ047	139.7	133.1	0	481.3	857.9	831.8	954.1	1926.3	3129.6
LPZ049	1396.5	2125.5	1496.9	4514.4	3629.8	5942.4	6898.6	3610.7	9214.2
LPZ051	264.6	610.7	205.1	826.3	1819.9	2243.8	3000.9	3400.7	2810.3
LPZ053	174.9	827.9	152	161.2	563.8	1149.7	1277.9	1243	1383.5
LPZ054	205.7	951	128.4	976.1	1901.4	1626.6	1265.8	1437.6	1328.8
LPZ055	135.2	389	168.5	420.2	524.3	1650.6	848.4	1200.6	914.2
LPZ056	190.2	323.3	229.5	439.9	664.2	1613.1	1014.2	1727.3	1126.2
LPZ057	87	199.9	180.1	2154	863.7	3059.1	2994.9	2696.3	2990
LPZ058	139.3	227.5	55.3	1695.1	902.5	2426.6	2195.6	1925.4	1598.2
LPZ059	173.4	289.6	189.4	891.7	759.7	1835.3	1332.9	962.5	1286.6
LPZ060	301	464.8	114.1	2296.5	2860.4	2786.6	2974.4	1629.6	2301.9
LPZ061	1212.2	1711.1	794.4	7468.5	5190.1	7957.5	5857.5	2819.8	3922.3
LPZ062	2078.9	3648.3	2499.3	14932.7	7691.9	9294.1	9213.3	3077.8	4850.3
LPZ063	641.6	984	2114.2	5547.2	3688.6	6191.3	4844.5	4058.7	4162.4
LPZ065	520.2	443.3	332.3	2720.4	1816	2848.5	3320.4	4501	3948.4
LPZ066	663.7	357	356.6	3458.6	2196.3	3567.6	3081.4	1325	2388
LPZ067	1469.5	2582.6	3152.4	8674.9	8080.1	9367.6	8556.2	4135	7240
LPZ069	211.4	283.6	0	1921.6	913.1	1567.5	1866.5	1043.3	2269.1
LPZ070	229.6	334.9	2.8	1659.3	1254.6	1681.6	1883.6	1360.7	2442
LPZ071	332.3	633	15.7	3126	2729.9	3290.2	2998	2011.7	2744.8
LPZ072	39	38.9	0	581.2	1401.7	1307.1	1089.7	710.4	1866.3
LPZ073	131.3	250.9	4.4	1176.4	2903.2	2356.7	1718.3	985.9	2700
LPZ074	92	116.5	0	355.6	1643	1041.3	1027.4	1042	2553.6
LPZ075	195.9	0	0	0	474.7	488.1	847.6	1488.4	2755
LPZ076	232.4	134.5	730.7	0	268.9	0	568.3	1007.4	2624.4
LPZ077	1143.1	2350.7	187.5	6551.1	5960.9	5520.2	7189.6	3483.6	7931.5
LPZ078	851.5	1021	873.3	3011.7	4619.7	5273.6	6408.3	3950.1	8831
LPZ079	281.6	779.7	315.9	1296.6	2065	2090.8	2287	2271.9	1824.5
LPZ080	1653.5	3124.5	3778.7	8321.1	7987.7	10470.3	8085.7	4454.9	8067.4
LPZ081	92.6	292.7	161.8	746.8	903	1558.5	1410.8	746.1	1230
LPZ082	123.2	430.5	240.1	1907.9	1283.9	2707.5	1801.7	948.9	1634

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FINNEGAN, HENDERSON,
FARABOW, GARRETT,
& DUNNER, L.L.P.
1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPZ083	77.8	183.2	120.2	4010	2437.2	4390.6	3649.7	3983.1	7032.5
LPZ084	1272.3	956.1	1297.2	5881	4505.3	10642.2	9798.6	3938.5	8446.3
LPZ085	321	466.2	457.6	4324.8	4008.4	6890.5	4599.7	5672	10082.2
LPZ086	1529.6	3587.2	3236.8	10729.4	10010.2	10739.2	10634.9	4674.2	11980.7
LPZ089	614.3	500.4	601.9	4196.2	3890.5	4405.8	4331.9	3066.9	3960.3
LPZ090	643.8	1177.5	1315	4017.8	4456.2	6394.5	4824.4	3000.1	3538.3
LPZ091	1006.7	1754.2	4090	11615.8	11728.5	16837.8	14461.9	5005.1	14726.4
LPZ092	419	528.6	1336.8	4158.4	3568.1	8393.4	8192	4638.4	3939.4
LPZ093	162.2	453	90.9	1436.5	899.2	2218.6	1798	741.8	1789.8
LPZ094	123.1	197.1	0	1355.7	779.4	1360.5	1713.8	794.4	1597.8
LPZ095	94	130.6	3.5	1099.9	737.4	558.3	1473.4	871.4	1809.3
LPZ096	314.3	327.5	22.1	2574.2	1620.9	2748.1	2533.9	1858.4	2979.9
LPZ099	231.7	359.8	6.2	1456.9	1335.7	1672.4	2170.8	2160.8	2755.8
LPZ100	375.6	650.4	136.7	2834	2518.6	3053.2	3159.8	2841.2	3453.7
LPZ101	217.1	425.7	11.8	2769.3	3312.6	2556.3	5262.5	1501.2	2947.3
LPZ102	294.3	289.2	55	1803.6	2764.5	2532.5	2613.4	2447.6	3377.6
LPZ103	224.2	92.8	17	989	1850.6	1643.7	2303.4	3729.5	4029.5
LPZ106	328.4	158	57.5	912.5	1239.6	1214.5	1669.6	2062.3	4720
LPZ107	25137.4	28865.6	19438.9	43316.7	75674.1	58296.4	45927	3332.1	64391.6
LPZ108	1132.8	2084.1	330.6	4299.2	3629.8	4480	6406.5	3235.2	9993.6
LPZ109	548.8	1356.1	417.7	3237.9	2581.9	3177.5	3977.1	1874.2	4107.7
LPZ110	379.7	1132.3	220	3941.9	2720.7	4103.6	3563	2245.7	3031
LPZ111	157.5	383.2	200.3	1188.3	749.8	1675.7	1926.1	1685.1	1655.3
LPZ112	332.1	522.9	220.7	2950.9	2223.9	2257.5	2856.4	2632.8	2711.8
LPZ114	590	151.8	217	4659.6	3824.5	6848.2	7228.9	2831.3	9446.9
LPZ115	6268.6	3368.3	8724.6	25695	19481.5	33011.8	32267.9	2903.4	52760.4
LPZ116	891.2	766.7	1481	6455.1	3684.7	5597.5	8456.7	1682.9	10139.2
LPZ117	529.8	826.6	126.5	3706.8	2663	2897.5	3996.1	1807.3	2635.2
LPZ118	437.8	628.1	122.1	3903.5	3245.2	3529.9	3500.1	3506.1	2867.9
LPZ119	331.3	755.1	83.1	3761.2	4072.6	4024.9	3449.9	3742.2	2533.9
LPZ120	196.5	796	181.4	4219.4	3297.7	4322	4539.3	2622.7	3763.6
LPZ122	154.4	208.4	158	2332.3	1468	3044	2838.8	2112.5	2323.6
LPZ124	172.9	420.1	136.6	2319.5	1539.3	1722.7	2453.6	3109.1	2297
LPZ126	446.5	604.2	187.3	3859.4	3120.8	2816.9	3324	2181.4	3237.7
LPZ127	439.3	499.4	53.5	3781.8	3083.3	3769.8	3848.4	1729.6	2902.2
LPZ128	1022.3	1063.8	447.9	3904.9	3753.5	5579.6	4534.2	2133.1	5843.6
LPZ131	249.6	373.8	27.3	2170.1	1551.6	1611.4	3077.3	2946	2409.5
LPZ133	325.3	328.7	42	2706.9	2358.1	2131.3	3257.2	2598.7	2144.3
LPZ136	263.6	384.1	0.9	2377.3	3386.4	2044.7	2726.4	2398.2	2570.6
LPZ137	351.6	402.6	91.9	3435.9	3122.8	2406.9	3054.7	3392.1	3216.6
LPZ138	1047.7	936	530.3	3920	3091.2	2507.9	4249.5	3109.9	4758.4
LPZ140	379.9	456.6	105.6	1936.7	3674	2908.4	3678.1	3663.2	4481.7
LPZ141	715.4	1341.8	536.4	4712.8	3615.6	3746	4815.5	4533	8229.3
LPZ143	3251.1	4810.8	2848.5	9675.1	8289.6	9486.6	12270.6	4424.9	28251.9
LPZ144	386.2	1338.3	294.1	3433.8	3015.7	3333.7	4618.9	3699.7	6825.1
LPZ145	277.5	1064	536.5	3072.3	1155.6	2977.7	3188.2	7388.2	3013.6
LPZ146	128.5	362.8	139.5	2224.4	1364	2125.6	2428.3	3465.8	2351.1
LPZ147	266.5	544.2	241.3	3318.1	2241.9	2162.6	2908.8	3252.6	2525.6
LPZ148	725.8	725.5	290.2	5002.2	3682.1	6542.3	6927.9	2903.1	10410.9
LPZ149	2492.7	3102.7	1052.7	8980.9	7669.2	7185.3	9921	7375.4	12848.8

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1300 I STREET, N. W.
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202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPZ150	5257.3	7586.3	3221.3	15156.2	12776.8	7401.2	14686.5	1570	20635.9
LPZ151	1384	2049.2	1128.3	5576.7	3853.7	3780.3	7227.3	3206.7	7702.7
LPZ152	975.8	1300.2	546.4	5096.1	4344.9	4302.5	4960.3	1566.2	4223.4
LPZ153	13378.6	22235.1	10073.1	33495.1	50802.7	28291.5	29602.5	3224.1	40232.7
LPZ154	663.3	738	430.3	3847.3	3880.2	6253.9	4707.7	5341.9	3393.8
LPZ155	1121.7	612.7	748	3902.3	4289	4676	5328	6964.2	5353.5
LPZ157	1157	957.9	762.2	4218.8	4266.6	3777.2	4583.7	5017.5	4396.6
LPZ158	13278.5	17582.9	9898.7	32456.5	42805.1	24534.6	31442.6	4152.5	36015.3
LPZ162	3407.5	5943.1	5126.6	10324	11710.9	7727.6	7572.2	2312.6	9394.1
LPZ165	1419.4	1550	693	4519.9	3692.9	6102.1	5617.1	3061.3	4706.4
LPZ166	2642.1	3504.9	1288.6	7134.8	6994.5	5170.5	10453.3	4932.9	15993.7
LPZ167	980.4	1518.1	564.7	4902.6	4803.7	3343.6	4869.5	4421.2	6582.2
LPZ169	621.8	792.7	93.4	3562	4266.3	1794.9	3496.3	4238	3143.7
LPZ170	1009.3	1405.3	695.2	5793.7	4469.2	4952.7	6239.7	3914.1	6782.3
LPZ171	1064.6	968.6	1050.7	4110.8	3903.7	5467.2	5659	3164.1	6795.3
LPZ172	1233.3	1113.3	401.8	4207.9	7922	8417.5	10419.2	7983.5	15065.2
LPZ173	3333.8	5236.8	6072	9552	8880	8653.2	13461.6	2408.7	25719.1
LPZ174	486.7	1263.6	143.3	3318.2	2027	3632.3	4245.3	6086.4	8781.2
LPZ175	594.7	1487	520.8	3051.5	3610.8	1846.4	3642.9	4048.5	4329.5
LPZ177	167.3	481.7	234.5	1955.9	1139.2	907.8	1452.9	4462.5	1762
LPZ179	1231.4	1583.2	835.8	5029.7	3654	3871.7	3248.8	2741.9	2853.2
LPZ181	2259.5	4282.9	774.8	8911.6	8788.6	6833.3	5825.5	3398	3922.8
LPZ182	1194.7	2289.6	673.8	8220.3	5601.2	5869.3	5572	1808.4	7607.9
LPZ186	6255.6	6866.5	6841.1	24861.8	16742.4	23502.2	17304.6	1750.4	27328.9
LPZ189	27581.8	34787.4	31889	45673.7	106688	95043.9	46998.5	3548.1	67943.9
LPZ194	673.9	904.9	528.7	4064.5	3530.2	3160.6	5095.2	4531.1	3492.1
LPZ195	898.9	889.6	675.7	5606.3	4004.3	5230.5	5721.4	4908.1	4940.9
LPZ196	1073.7	1935.1	558.2	3941.1	3672.6	3681.6	5977.8	3059.7	5050.3
LPZ197	488.4	522.5	386.6	2613.4	1684.4	3541.4	3507.4	4980.8	2763.1
LPZ198	575.6	733.1	299.6	4152.3	2411	2916.8	3872.4	6530.7	2931.8
LPZ199	390.7	442.5	222.4	2704	2176.2	3159.7	2957.1	5357.6	2983.4
LPZ201	2255.7	3876.6	347.6	10222.9	6897.7	6294.3	7324.7	3549	3857
LPZ202	25939.2	34864.8	28937	43395.9	85136	71116.8	38688.5	2676.2	14449.1
LPZ203	4917.3	4458.1	2603.2	10348.3	6571.1	8325.7	11034	5453.1	6598
LPZ204	27637.2	31853.9	22475.7	43983.9	89520.6	46504.2	44333.5	7963.8	58054.1
LPZ205	1184	1084.2	327.7	3901.8	4402	3125	4598.2	4501.5	4714.2
LPZ206	1309.8	1509.5	367.3	3961.5	3983.3	3079.6	4196.2	3641.4	3247.6
LPZ207	27569.1	30446.2	27094.6	45211.6	90196.1	58153.8	46488.1	9879.3	64709.2
LPZ208	22722	28208.9	30019.5	40314	74354.1	37339	33919.6	3989.8	56683.6
LPZ210	1015.1	1789.8	196.8	5006.3	6159.7	3067.8	4944	4347.5	6846.4
LPZ211	277	327.3	519.4	2540.7	1788.5	3048.6	1110.8	2577.4	3506.6
LPZ212	1095.5	865.5	930.6	4051.6	4491.6	2857.6	6348.1	4078.7	16174.9
LPZ213	376.6	539.3	339.6	2503.1	1540.8	1333.7	3082.2	6024.3	4163.1
LPZ214	137.5	306.1	190.1	1915.6	866.1	1280.9	1240.8	6372.4	2111.8
LPZ215	3519.4	3120.9	3300.9	16939.5	15489.1	10948.6	12502	3515.1	16236.4
LPZ216	26761.3	34226.4	28477.9	42274.8	67630.3	41420.3	36331.4	1433.8	17109.4
LPZ217	15563.1	21739.4	12259	26824.9	34266.3	9429.4	28156.7	1339.2	41568.4
LPZ219	2404.9	3704.5	2084	8575.1	8573.2	6237	11757	3255.4	13484.9
LPZ220	3617.2	6998.6	7957.2	13960	9400.8	3432.3	10805.5	3551.7	12867.4
LPZ221	482.6	478	1405.6	3296.5	3079.8	3312.5	4143	4429.4	3267.3

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FINNEGAN, HENDERSON,
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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPZ222	318.3	524.5	406.6	3011.7	2309	3811.8	4199.4	5319.9	3292.3
LPZ223	367.7	633.2	437.7	2752	1970.3	3767.4	2514.2	3672.3	2163.1
LPZ224	337.9	1030.2	317.2	2701.2	1798.7	7393.6	2962.5	7876	3353.7
LPZ225	3288.1	3590.3	2912	8781.8	7400.7	2317.1	11370.2	3186.6	22244.6
LPZ226	325.6	361.4	128	2467	1263.7	10190.1	1636.3	3808.8	1166.9
LPZ227	2175.5	6375.8	458.8	6316.2	6632.1	9013.9	6614.3	3901.2	2588.2
LPZ228	2638	3701.7	500.1	5991	4819.8	5747.8	7102.5	3182.5	4185.4
LPZ231	1631.7	2090.4	260.7	5811.5	4749	2530.8	5033.1	3191.3	3810.5
LPZ233	1596.6	1223	296.6	4355.6	3818.9	2988.8	3749	3324.7	3855.2
LPZ234	1734.3	1479.2	219.6	5058.5	4614.4	2034.9	4992.1	1979.9	5152
LPZ235	626	635.9	185.9	4066.8	3255.5	4035.7	3368.7	2880.8	3643.5
LPZ237	1677.8	1385.3	847.4	4536	3702.8	2943.6	4886.5	2307.8	5136.8
LPZ239	673.4	407.8	245.8	2981.9	3199.2	2781.6	4235.6	2342.6	4863.7
LPZ240	387	247.4	254.8	2075.8	2317.4	2894	2721.7	2054.5	4317.9
LPZ241	258.3	337.8	110.9	3503.1	3829.6	22593.5	1889.5	1315.9	8842.6
LPZ242	4315.9	2560.2	22.5	12510.2	12605.3	2345.2	16197.1	1114.8	39684.4
LPZ243	174.8	274.4	23.1	2193.6	346.2	2395.7	1366.5	2568.2	3103.8
LPZ244	417.5	269.1	3458.5	3545.1	1831	2834.7	1781.1	7589.2	5662.7
LPZ246	889.5	918.7	2302.7	3920.3	3228.9	4409.3	3536	1258.8	2645.3
LPZ247	1203	2088.9	46.7	4956.9	4253.2	3559.7	4570.8	1702.6	3350.6
LPZ248	973.3	1338.1	86.2	3977.4	4392.8	2033	4094.9	2062.6	4279.9
LPZ249	361.3	324.3	206.7	1948.6	1764.3	2098.7	2762.1	1643	2862.4
LPZ250	267.6	487.8	118.7	2690.4	1522	2989	3121	1928.9	1809.7
LPZ251	245	279.7	168.5	1409.9	555	9932.3	2552.5	3050.3	1371.1
LPZ255	2021.3	2488.5	334.1	7289.5	7773.7	1269.1	9020.3	4492.4	10134.6
LPZ256	67.1	72.2	296.7	412.2	229.8	922.7	570.3	5040.6	1263.9
LPZ257	167.3	146.9	482.6	521.8	102.5	2699.4	599.8	2362.1	1553.4
LPZ258	247.5	236.5	69.7	1429.8	974.6	971.9	2668.7	2990.8	3445.9
LPZ260	98.1	188.8	463.1	377.1	337.2	880	808.9	1552	1084.6
LPZ261	73.7	20.5	386.3	1143.6	50.3	4443.8	903.3	2309	1341.6
LPZ264	482.7	528.5	1151.3	3659.7	1972.6	9892.4	2831.4	1584.4	3208
LPZ265	534.6	647	457.6	4473	4089.9	656	5899.6	2972.2	5649.8
LPZ266	16.9	61.2	1062.3	876.1	1183.4	1624.3	663.3	622.4	1609.7
LPZ268	143.7	142.9	255	1983.5	810.3	9809.8	1293.5	1757.3	2177
LPZ269	1747.5	1271.8	1636.4	7364.1	5108.7	6903.3	11401.2	3774.1	14643.8
LPZ270	373.8	77.9	1901.2	5015	3872.6	3485.9	5621.1	4284.8	5197.8
LPZ271	705	473.1	315.6	2863.8	2625.4	2120.5	4048.2	1424.9	4291.1
LPZ272	2809.4	2423.8	300	5056.2	2463	3534.6	3496.9	609.7	3996.8
LPZ273	219.8	162.4	242.4	90.2	130.2	3251.3	166	1193.5	1836.5
LPZ274	489.2	367.7	284.6	991	1104.2	395.9	2282.3	747.2	4535.7
LPZ275	93.5	140	156.8	433.3	217.1	0	837.9	1056.2	2352.3
LPZ276	53	109.7	106.8	0	0	0	369.1	1303.6	1897.6
LPZ277	105.9	159.4	68.7	0	0	230.1	236.2	706.1	1337.9
LPZ278	65.7	48.3	156.4	0	0	1788.2	406.3	1442.3	1564.1
LPZ279	214.7	212.2	75.3	1356.3	790.8	5213.3	1722.4	496	2426.2
LPZ280	156.2	247.7	1553.6	3510.5	2515.1	289.7	3182.1	612.7	3123.7
LPZ281	34.6	92.1	73	0	0	1648.3	565.5	522.8	543.3
LPZ282	200.9	187.7	218.1	536.6	205.9	7324.8	1145.4	2977.5	957.5
LPZ283	1833.5	1880	775.8	3303.2	5113.2	527.6	5281.2	324.5	3806.8
LPZ284	215	0.6	148.8	0	29.6	848	408.4	148.8	1294.3

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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE II

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPZ286	219.7	21.9	13.6	234.9	78.6	2703.6	198.4	947.9	1233.2
LPZ287	112.6	126.2	36.5	1170.3	459.9	306.3	157.5	1173.7	1821.3
LPZ288	23.6	62.2	37.5	774.1	639.3	792.6	715.8	1422.6	1169
LPZ289	44.1	13.1	107.4	323.4	95	9975.4	889.5	2240.6	1894.9
LPZ290	1324.7	1572.4	1838	6941.6	4616.9	2995.3	11538.8	407.1	12699.5
LPZ293	45.2	246.3	145.6	2785.5	1923.1	0	3185.6	0	3550.4
LPZ294	0	19.8	0	403.3	280.4	89.1	785.9	551.6	1378.4
LPZ295	40	24.5	0	169.9	26	1324.9	1058	848.8	1406.5
LPZ297	385.6	127.6	17.4	1238.5	941.5	0	2680.9	2084.3	4065.3
LPZ299	106.9	36.2	0	0	926.2	0	1060.7	1854.9	1575.9
LPZ300	73.2	93.2	80.2	0	1143.6	1053.3	1034.5	2304.9	2120.8
LPZ301	126.2	0	5.8	161.2	1245.7	516.3	1612	761.3	2826.1
LPZ303	83.1	488.8	98.6	0	73.5	979.9	538.7	510.7	1214.7
LPZ304	213.7	498.3	137.6	1028.6	0	5405.8	860	2212.1	2201
LPZ306	1439.4	1735.3	2526.4	4212.7	3140.4	2090.1	8128.5	4874.6	14413.9
LPZ307	534.1	710.5	515.5	2785.3	734	0	2137.3	1692.8	3540.3
LPZ308	116	304.4	137.7	151.8	28.2	364.2	621.1	631.4	851.2
LPZ309	80.1	137.2	92.7	0	0	2648.1	529.4	192.6	735
LPZ310	430.8	584.9	799.2	1887.2	1887.1	6161.2	2974.3	3575	2426.6
LPZ311	690.5	995.7	208.4	3725.8	2843.8	0	4329.3	3620.8	4170.1
LPZ312	109.8	334.2	34	72.5	4.5	1489.3	140.1	431.6	744.8
LPZ314	26.5	200.1	3.3	181.2	0	1231.5	331.5	440.1	804.6
LPZ315	305.8	211.3	147.5	811.2	1008.1	3797	2231.8	1438.8	1881.8
LPZ318	621.3	715	337	3488.2	2480.9	781.9	4326.1	4824.7	6969.2
LPZ320	214.8	92.2	9.9	1170.9	54.5	4501.5	1122.3	1169.4	1696.6
LPZ321	880.4	755.2	1899.3	6166.2	5105.8	411.6	6096.5	4853.6	6057.2

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1300 I STREET, N. W.
WASHINGTON, DC 20005
202-408-4000

TABLE III

LSC Media	Multiplication Media		Maturation Media
Components (mg/L)	16	1133	923
NH_4NO_3	603.8	603.8	200.0
KNO_3	909.9	909.9	454.95
KH_2PO_4	136.1	136.1	136.1
$Ca(NO_3)_2 \cdot 4H_2O$	236.2	236.2	59.05
$MgSO_4 \cdot 7H_2O$	246.5	246.5	246.5
$Mg(NO_3)_2 \cdot 6H_2O$	256.5	256.5	256.5
$MgCl_2 \cdot 6\ H_2O$	101.7	101.7	101.7
KI	4.15	4.15	4.15
H_3BO_3	15.5	15.5	7.75
$MnSO_4 \cdot H_2O$	10.5	10.5	10.5
$ZnSO_4 \cdot 7\ H_2O$	14.4	14.4	14.4
$NaMoO_4 \cdot 2\ H_2O$	0.125	0.125	0.125
$CuSO_4 \cdot 5\ H_2O$	0.125	0.125	0.125
$CoCl_2 \cdot 6\ H_2O$	0.125	0.125	0.125
$FeSo_4 \cdot 7\ H_2O$	6.95	6.95	41.7
Na_2EDTA	9.33	9.33	55.9
Sucrose	30,000	30,000	--
Maltose	--	--	20,000
myo-Inositol	1,000	1,000	100
Casamino acids	500	500	500
L-Glutamine	450	450	450
Thiamine•HCl	1.0	1.0	1.0
Pyridoxine•HCl	0.5	0.5	0.5
Nicotinic acid	0.5	0.5	0.5
Glycine	2.0	2.0	2.0
2,4-D	1.1	1.1	--
BAP	0.45	0.45	--
Kinetin	0.43	0.43	--
Polyethylene glycol	--	--	130,000
ABA	--	5.2	5.2
Gelrite	*2,500**	*2,500**	2,500
pH	5.7	5.7	5.7

*For solid media only

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TABLE IV

Clone #	Homology	Description	ID with Arabidopsis	Score	E-value
PC04B12 ('LEC' in figure)	Lotan et al.. 1998. Arabidopsis *LEAFY COTYLEDON* 1 is sufficient to Induce Embryo Development in Vegetative Cells. Cell 93:1195-1205	Required for embryo maturation & Cotyledon identity. Ectopic expression induces embryonic differentiation traits in transgenic seedlings.	79%ID, 93% + ve over 96aa	171	7e-44
ST17B05 ('PLK' in figure)	PICLKE/CDH3, Chromatin remodelling . Ogas et al. 1999. PICKLE is a CHD3 chromatin-remodeling factor that regulates the transition from embryonic to vegetative development in *Arabidopsis*. PNAS. 96(24): 13839-13844	The *pickle* mutants express embryonic traits after germination. Represses lec expression	50% ID, 74% + ve over 155aa	166	1e-41
PC08C06 ('FIE' in figure.)	FIE, fertilization-independent endosperm protein. Ohad, et al 1999.Mutations in FIE, a WD polycomb group gene, allow endosperm development without fertilization. Plant Cell 11 (3), 407-416	*Fie* mutants initiate endosperm development w/o fertilization	61% ID 75% +ve over 67aa	92	8e-20

Table 4. Description of clones used in hybridization study shown in Figure 9.

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TABLE V

Cell Lin (Stage of Development)	**488** (Liquid Suspension Culture: Stage 1-3)	**499** (Liquid Suspension Culture: Stage 1-3)	**499** (Liquid Suspension Culture: Stage 1-3)	**500** (Liquid Suspension Culture: Stage 1-3)	**500** (Liquid Suspension Culture: Stage 1-3)	**260** (Stage 7)	**260** (Stage 9)
Media	1133	16	1133	16	1133	Maturation	maturation
# Embyros	**49.5**	**118.5**	**129.5**	**187.75**	**147**	**Na**	**na**
'FIE'	**++++**	**+**	**+++**	**+++**	**+++**	**+++**	**+++**
'LEC'	**++**	**++**	**+++**	**++**	**++++**	**+**	**+**
'PKL'	**++++**	**+**	**+++**	**+++**	**+++**	**+++**	**+++**

Table 5. Table of data from Fig. 9a & b. Numbers (488, 499, 500, 260) refer to different cell lines. Liquid Suspension Culture contains early-stage embryos (stage 1-3) Embryo number refers to the number of late-stage (stage 8-9) embryos produced by each cell line when matured according to Pullman and Webb (1994). + = low expression, ++ = medium level of mRNA, +++ = high level of mRNA, ++++= very high level of mRNA. Circles around certain + signs, see text. Na = not applicable. Levels of mRNA are relative and refer to the experiment depicted in Fig. 9a &b.

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